

BLASTN 2.2.13 [Nov-27-2005]

RID: 1143643332-20069-153143060667.BLASTQ1

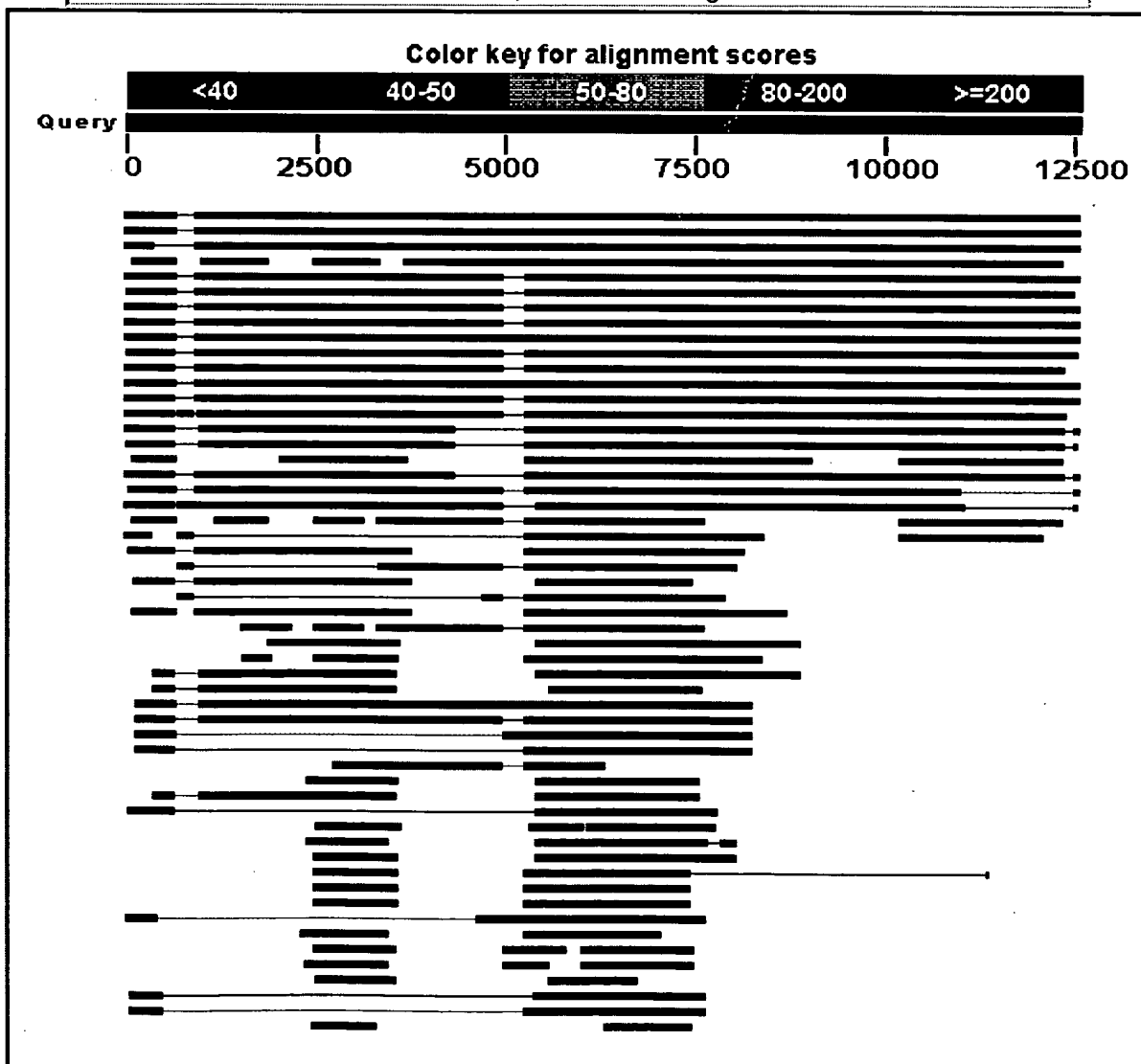
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,819,973 sequences; 16,928,533,343 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=12611

Distribution of 193 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Sequences producing significant alignments:	Score (Bits)	E Value
gi 323205 gb M31182.1 BVDCG Bovine viral diarrhea virus 1-NADL,	2.140e+04	0.0
gi 7960753 emb AJ133738.1 BVI133738 Bovine viral diarrhea virus	2.132e+04	0.0
gi 9049956 gb AF268278.1 AF268278 Pestivirus type 1, complete ge	2.131e+04	0.0
gi 55724858 emb AJ781045.1 Bovine viral diarrhea virus parti...	1.573e+04	0.0
gi 7960755 emb AJ133739.1 BVI133739 Bovine viral diarrhea vir...	1.333e+04	0.0
gi 71727706 gb DQ088995.1 Bovine viral diarrhea virus 1 stra...	1.182e+04	0.0
gi 289507 gb M96751.1 BVDPOLYPRO Bovine viral diarrhea virus ...	8981	0.0
gi 3661565 gb AF091605.1 AF091605 Bovine viral diarrhea virus st	8937	0.0
gi 28071149 dbj AB078951.1 Bovine viral diarrhea virus-1 gen...	8911	0.0
gi 2789676 gb AF041040.1 AF041040 Pestivirus type 1 polyprotein	8841	0.0
gi 2149468 gb U86600.1 PTU86600 Pestivirus type 1 noncytopathic	6423	0.0
gi 28071151 dbj AB078952.1 Bovine viral diarrhea virus-1 gen...	6344	0.0
gi 28071147 dbj AB078950.1 Bovine viral diarrhea virus-1 gen...	6274	0.0
gi 2149466 gb U86599.1 PTU86599 Pestivirus type 1 cytopathic gen	5489	0.0
gi 9836967 gb AF220247.1 AF220247 Bovine viral diarrhea virus-1,	5214	0.0
gi 1518835 gb U63479.1 BVU63479 Bovine viral diarrhea virus 1...	5214	0.0
gi 323222 gb M96641.1 BVDP12510A Bovine viral diarrhea virus ...	4745	0.0
gi 37693100 emb AJ585412.1 Bovine viral diarrhea virus VEDEV...	4641	0.0
gi 76781922 gb AF526381.3 Bovine viral diarrhea virus 1 strain	4501	0.0
gi 323229 gb M96687.1 BVDP Bovine viral diarrhea virus strai...	4307	0.0
gi 642600 gb L35852.1 BVDP125E Bovine viral diarrhea virus (s...	3988	0.0
gi 39725568 dbj AB111966.1 Bovine viral diarrhea virus 190cp...	3917	0.0
gi 323220 gb M62430.1 BVDNCP1 Bovine viral diarrhea virus NCP...	3651	0.0
gi 39725570 dbj AB111967.1 Bovine viral diarrhea virus T-20 ...	3498	0.0
gi 3746673 gb AF078534.1 AF078534 Pestivirus type 1 strain Si...	3485	0.0
gi 84180866 gb DQ323915.1 Bovine viral diarrhea virus 1 stra...	3434	0.0
gi 323207 gb M62431.1 BVDCP1 Bovine viral diarrhea virus CP1 ...	3216	0.0
gi 1628570 gb U63512.1 BVU63512 Bovine viral diarrhea virus c...	3186	0.0
gi 642598 gb L35851.1 BVDP125D Bovine viral diarrhea virus (s...	3097	0.0
gi 14579251 gb AF321452.1 AF321452 Bovine viral diarrhea viru...	3083	0.0
gi 39725566 dbj AB111965.1 Bovine viral diarrhea virus 190nc...	3029	0.0
gi 14579249 gb AF321451.1 AF321451 Bovine viral diarrhea viru...	3011	0.0
gi 2073011 gb U96334.1 PTU96334 Pestivirus type 1 strain R193...	2665	0.0
gi 77799881 dbj AB111964.2 Bovine viral diarrhea virus 839cp...	2658	0.0
gi 289505 gb L12455.1 BVDSINGER Bovine viral diarrhea virus RNA	2636	0.0
gi 77799879 dbj AB111963.2 Bovine viral diarrhea virus 839nc...	2619	0.0
gi 77799877 dbj AB111962.2 Bovine viral diarrhea virus 799cp...	2615	0.0
gi 77799875 dbj AB111961.2 Bovine viral diarrhea virus 799nc...	2603	0.0
gi 3746675 gb AF078535.1 AF078535 Pestivirus type 1 strain Ne...	2588	0.0
gi 22252901 gb AY121916.1 Pestivirus type 1 isolate i-N-CTHB...	2508	0.0
gi 14113964 gb AF049221.2 AF049221 Bovine viral diarrhea viru...	2396	0.0
gi 2997667 gb AF052303.1 Pestivirus type 1 strain Bega polyprot	2377	0.0
gi 14112656 gb AF049222.2 AF049222 Bovine viral diarrhea viru...	2377	0.0
gi 14209816 gb AF255049.1 AF255049 Bovine viral diarrhea viru...	2375	0.0
gi 3746677 gb AF078536.1 AF078536 Pestivirus type 1 strain Or...	2362	0.0
gi 2997669 gb AF052304.1 Pestivirus type 1 strain Trangie polyp	2300	0.0
gi 487966 gb U03912.1 BVU03912 Bovine viral diarrhea virus polyp	2152	0.0
gi 2465191 gb U80885.1 PTU80885 Pestivirus type 1 polyprotein (L	2102	0.0
gi 14579247 gb AF321450.1 AF321450 Bovine viral diarrhea viru...	2080	0.0
gi 3885462 gb AF058699.1 AF058699 Bovine viral diarrhea virus...	2078	0.0
gi 28564452 emb AJ544865.1 PTY544865 Bovine viral diarrhea vi...	2041	0.0
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gi 28564450 emb AJ544864.1 PTY544864 Bovine viral diarrhea vi...	1964	0.0
gi 454348 gb U00891.1 PTU00891 Border disease virus polyprotein	1882	0.0
gi 3859507 gb AF083348.1 AF083348 Pestivirus type 1 strain Si...	1733	0.0

gi 15282441 gb AF144617.2 AF144617	Pestivirus giraffe-1 H138 com	1652	0.0
gi 34596505 gb AY182137.1 AY182136S2	Pestivirus type 1 strain CP	1650	0.0
gi 11094035 gb AF312856.1	Pestivirus isolate Hay 87/2210 non...	1568	0.0
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gi 59624984 gb AY911671.1	Bovine pestivirus Ind S1456 polyprote	1393	0.0
gi 59624986 gb AY911672.1	Bovine pestivirus Ind S1226 polyprote	1382	0.0
gi 992589 emb Z54185.1 BVDGP04	Bovine viral diarrhea virus (TGAC	1380	0.0
gi 1256840 gb U53408.1 BVU53408	Bovine viral diarrhea virus NS3	1317	0.0
gi 1703497 gb U70263.1 BDU70263	Border disease virus strain BD31	1291	0.0
gi 2073009 gb U96333.1 PTU96333	Pestivirus type 1 strain R193...	1286	0.0
gi 59624982 gb AY911670.1	Bovine pestivirus Ind S1449 polyprote	1277	0.0
gi 606399 gb L38697.1 BVDGP53SGP	Bovine viral diarrhea virus ...	1236	0.0
gi 484115 gb L07496.1 BVDGP53ENV	Bovine viral diarrhoea virus...	1192	0.0
gi 15282443 gb AF144618.2 AF144618	Pestivirus reindeer-1 V60-Kre	1190	0.0
gi 7637400 dbj AB033752.1	Pestivirus type 1 genomic RNA for ...	1153	0.0
gi 557924 gb S71487.1	gp48=glycoprotein [bovine viral diarrh...	1136	0.0
gi 84374633 gb DQ328323.1	Bovine viral diarrhea virus 1 stra...	1096	0.0
gi 6049233 gb AF144611.1 AF144611	Bovine viral diarrhea virus...	1081	0.0
gi 5420140 emb Y19123.1 BDV19123	Bovine viral diarrhea virus ...	1081	0.0
gi 30962158 emb AJ558196.1 BVI558196	Bovine viral diarrhea vi...	1070	0.0
gi 67772267 gb DQ067603.1	Bovine viral diarrhea virus 1 isol...	1053	0.0
gi 67772263 gb DQ067601.1	Bovine viral diarrhea virus 1 isol...	1031	0.0
gi 67772265 gb DQ067602.1	Bovine viral diarrhea virus 1 isol...	1026	0.0
gi 2981424 gb AF049226.1 AF049226	Pestivirus type 1 strain Gl...	933	0.0
gi 6049236 gb AF144614.1 AF144614	Bovine viral diarrhea virus...	915	0.0
gi 2073007 gb U96332.1 PTU96332	Pestivirus type 1 strain R193...	913	0.0
gi 2981420 gb AF049224.1 AF049224	Pestivirus type 1 strain Tr...	881	0.0
gi 6049232 gb AF144610.1 AF144610	Bovine viral diarrhea virus...	878	0.0
gi 11935042 gb AF302463.1 AF302463	Pestivirus type 1 strain SD-1	857	0.0
gi 1698911 gb U75982.1 PTU75982	Pestivirus type 1 E0/E1 gene, pa	835	0.0
gi 323223 gb M96640.1 BVDP12580A	Bovine viral diarrhea virus n...	791	0.0
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gi 32746263 gb AY323893.1	Bovine viral diarrhea virus 1 isol...	730	0.0
gi 1009372 emb Z54332.1 BVD125IN2	Bovine viral diarrhea virus...	728	0.0
gi 61817276 gb AY845225.1	Bovine viral diarrhea virus 1-NADL...	715	0.0
gi 32746156 gb AY323892.1	Bovine viral diarrhea virus 1 isol...	713	0.0
gi 3786386 gb AF039181.1 AF039181	Pestivirus type 1 strain BVDVN	712	0.0
gi 5101889 emb AJ241231.1 BVI241231	Bovine viral diarrhea vir...	695	0.0
gi 5101917 emb AJ241245.1 BVI241245	Bovine viral diarrhea vir...	689	0.0
gi 5101895 emb AJ241234.1 BVI241234	Bovine viral diarrhea vir...	689	0.0
gi 5101887 emb AJ241230.1 BVI241230	Bovine viral diarrhea vir...	689	0.0

Alignments

> ☐ gi|323205|gb|M31182.1|BVDCG **BVD** Bovine viral diarrhea virus 1-NADL, complete gen
Length=12573

Score = 2.140e+04 bits (11589), Expect = 0.0
Identities = 11670/11684 (99%), Gaps = 6/11684 (0%)
Strand=Plus/Plus

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Query	6506	ACTGCCACGCCAGCAGGGTCGGTGACCACAACAGGTCAAAAGCACCCAATAGAGGAATTC	6565
Sbjct	6470	6529
Query	6566	ATAGCCCCCGAGGTAATGAAAGGGGAGGATCTTGGTAGTCAGTTCCTTGATATAGCAGGG	6625
Sbjct	6530	6589
Query	6626	TTAAAAATACCAGTGGATGAGATGAAAGGCAATATGTTGGTTTTTGTACCAACGAGAAAC	6685
Sbjct	6590	6649
Query	6686	ATGGCAGTAGAGGTAGCAAAGAAGCTAAAAGCTAAGGGCTATAACTCTGGATACTATTAC	6745
Sbjct	6650	6709
Query	6746	AGTGGAGAGGATCCAGCCAATCTGAGAGTTGTGACATCACAATCCCCCTATGTAATCGTG	6805
Sbjct	6710	6769
Query	6806	GCTACAAATGCTATTGAATCAGGAGTGACACTACCAGATTTGGACACGGTTATAGACACG	6865
Sbjct	6770	6829
Query	6866	GGGTTGAAATGTGAAAAGAGGGTGAGGGTATCATCAAAGATACCCTTCATCGTAACAGGC	6925
Sbjct	6830	6889
Query	6926	CTTAAGAGGATGGCCGTGACTGTGGGTGAGCAGGCGCAGCGTAGGGGCAGAGTAGGTAGA	6985
Sbjct	6890	6949
Query	6986	GTGAAACCCGGGAGGTATTATAGGAGCCAGGAAACAGCAACAGGGTCAAAGGACTACCAC	7045
Sbjct	6950	7009
Query	7046	TATGACCTCTTGACAGGCACAAAGATACGGGATTGAGGATGGAATCAACGTGACGAAATCC	7105
Sbjct	7010	7069
Query	7106	TTTAGGGAGATGAATTACGATTGGAGCCTATACGAGGAGGACAGCCTACTAATAACCCAG	7165
Sbjct	7070	7129
Query	7166	CTGGAAATACTAAATAATCTACTCATCTCAGAAGACTTGCCAGCCGCTGTTAAGAACATA	7225
Sbjct	7130	7189
Query	7226	ATGGCCAGGACTGATCACCCAGAGCCAATCCAACCTTGCATACAACAGCTATGAAGTCCAG	7285
Sbjct	7190	7249

Query	7286	GTCCCGGTCCTATTCCCAAAAATAAGGAATGGAGAAGTCACAGACACCTACGAAAATTAC	7345
Sbjct	7250	7309
Query	7346	TCGTTTCTAAATGCCAGAAAGTTAGGGGAGGATGTGCCCGTGTATATCTACGCTACTGAA	7405
Sbjct	7310	7369
Query	7406	GATGAGGATCTGGCAGTTGACCTCTTAGGGCTAGACTGGCCTGATCCTGGGAACCAGCAG	7465
Sbjct	7370	7429
Query	7466	GTAGTGGAGACTGGTAAAGCACTGAAGCAAGTGACCGGGTTGTCCTCGGCTGAAAATGCC	7525
Sbjct	7430	7489
Query	7526	CTACTAGTGGCTTTATTTGGGTATGTGGGTACCAGGCTCTCTCAAAGAGGCATGTCCCA	7585
Sbjct	7490	7549
Query	7586	ATGATAACAGACATATATACCATCGAGGACCAGAGACTAGAAGACACCACCCACCTCCAG	7645
Sbjct	7550	7609
Query	7646	TATGCACCCAACGCCATAAAAACCGATGGGACAGAGACTGAACTGAAAGAACTGGCGTCG	7705
Sbjct	7610	7669
Query	7706	GGTGACGTGGAAAAATCATGGGAGCCATTTAGATTATGCAGCTGGGGGACTGGAGTTT	7765
Sbjct	7670	7729
Query	7766	GTTAAATCCCAAGCAGAAAAGATAAAAACAGCTCCTTTGTTTAAAGAAAACGCAGAAGCC	7825
Sbjct	7730	7789
Query	7826	GCAAAAGGGTATGTCCAAAATTTCATTGACTCATTAAATTGAAAATAAAGAAGAAATAATC	7885
Sbjct	7790	7849
Query	7886	AGATATGGTTTGTGGGGAACACACACAGCACTATACAAAAGCATAGCTGCAAGACTGGGG	7945
Sbjct	7850	7909
Query	7946	CATGAAACAGCGTTTGCCACACTAGTGTAAAGTGGCTAGCTTTTGGAGGGGAATCAGTG	8005
Sbjct	7910	7969
Query	8006	TCAGACCACGTCAAGCAGGCGGCAGTTGATTTAGTGGTCTATTATGTGATGAATAAGCCT	8065
Sbjct	7970	8029
Query	8066	TCCTTCCCAGGTGACTCCGAGACACAGCAAGAAGGGAGGCGATTTCGTGCAAGCCTGTTC	8125
Sbjct	8030	8089
Query	8126	ATCTCCGCACTGGCAACCTACACATACAAACTTGGAATTACCACAATCTCTCTAAAGTG	8185
Sbjct	8090	8149
Query	8186	GTGGAAC-AGCCCTGGCTTACCTCCCTATGCTACCAGCGCATTAAAAATGTTACCCCA	8244
Sbjct	8150C.....	8209
Query	8245	ACGCGGCTGGAGAGCGTGGTGATACTGAGCACCACGATATATAAAACATACCTCTCTATA	8304
Sbjct	8210	8269
Query	8305	AGGAAGGGGAAGAGTGATGGATTGCTGGGTACGGGGATAAGTGCAGCCATGGAAATCCTG	8364
Sbjct	8270	8329
Query	8365	TCACAAAACCCAGTATCGGTAGGTATATCTGTGATGTTGGGGTAGGGGCAATCGCTGCG	8424
Sbjct	8330	8389
Query	8425	CACAACGCTATTGAGTCCAGTGAACAGAAAAGGACCCTACTTATGAAGGTGTTTGTAAG	8484
Sbjct	8390	8449
Query	8485	AACTTCTTGGATCAGGCTGCAACAGATGAGCTGGTAAAAGAAAACCCAGAAAAAATTATA	8544
Sbjct	8450	8509

Query	8545	ATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCCTGAGACTAATATACCACCTG	8604
Sbjct	8510	8569
Query	8605	TATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAAGTATCTGAGAGGACAGCAGGCAGA	8664
Sbjct	8570	8629
Query	8665	AACTTATTCACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGACTCACAAGGG	8724
Sbjct	8630	8689
Query	8725	AAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTACACAAGCAA	8784
Sbjct	8690	8749
Query	8785	ATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCTGCACCCTTTAGTTGTGAC	8844
Sbjct	8750	8809
Query	8845	TGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAAGTATTTGAGGGTAGAAACC	8904
Sbjct	8810	8869
Query	8905	AGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAAGTTACCAAA	8964
Sbjct	8870	8929
Query	8965	GTGGAGGAGAGCGGGCCTTTCCTATGTAGAAACAGACCTGGTAGGGGACCAAGTCAACTAC	9024
Sbjct	8930	8989
Query	9025	AGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCAAAGTTGGAA	9084
Sbjct	8990	9049
Query	9085	GGACAGGTAGAGCACTACTACAAAGGGGTACAGCAAAAATTGACTACAGTAAAGGAAAA	9144
Sbjct	9050	9109
Query	9145	ATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGGTAGCTAAG	9204
Sbjct	9110	9169
Query	9205	AGATATACTGGGGTCGGGTTCATGGTGCATACTTAGGTGACGAGCCCAATCACCGTGCT	9264
Sbjct	9170	9229
Query	9265	CTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTAAAAATGAAG	9324
Sbjct	9230	9289
Query	9325	AAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTCATCGAACTA	9384
Sbjct	9290	9349
Query	9385	GTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACCACATGGCTA	9444
Sbjct	9350	9409
Query	9445	GCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGAGAGAGAGTA	9504
Sbjct	9410	9469
Query	9505	ATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGACACGTCAGAG	9564
Sbjct	9470	9529
Query	9565	GTTGGGATCACAATAATTGGAAGGGAAACCCTGATGACAACGGGAGTGACACCTGTCTTG	9624
Sbjct	9530	9589
Query	9625	GAAAAAGTAGAGCCTGACGCCAGCGACAACCAAACTCGGTGAAGATCGGGTTGGATGAG	9684
Sbjct	9590	9649
Query	9685	GGTAATTACCCAGGGCCTGGAATACAGACACATACACTAACAGAAGAAATACACAACAGG	9744
Sbjct	9650	9709
Query	9745	GATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATCCATATCAAATAGGGCAAAG	9804
Sbjct	9710	9769

Query	9805	ACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCCAGGGAAATACGAGACTTGATG	9864
Sbjct	9770	9829
Query	9865	GCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTCGACCCTGAGCTGTCTGAAATG	9924
Sbjct	9830	9889
Query	9925	GTGGAATTTCAAGGGGACTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGTCTCGGGCAA	9984
Sbjct	9890	9949
Query	9985	CCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAGAAAAAGAT	10044
Sbjct	9950	10009
Query	10045	GTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTGGCCTTAAAA	10104
Sbjct	10010	10069
Query	10105	AATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCTAAAGCACTT	10164
Sbjct	10070	10129
Query	10165	GGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTATGCCATGAAG	10224
Sbjct	10130	10189
Query	10225	CTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCACTGTTTGAG	10283
Sbjct	10190T.....	10249
Query	10284	GAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATGGCATCAGCT	10343
Sbjct	10250	10309
Query	10344	TACCAATTGGCACAGGGTAAGTGGGAGCCCCTCGGTTGCGGGGTGCACCTAGGTACAATA	10403
Sbjct	10310	10369
Query	10404	CCAGCCAGAAGGGTGAAGATACACCCATATGAAGCTTACCTGAAGTTGAAAGATTTCATa	10463
Sbjct	10370	10429
Query	10464	gaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCACAACAAATGG	10523
Sbjct	10430	10489
Query	10524	ATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTCAACCCAGGG	10583
Sbjct	10490	10549
Query	10584	AAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAACCACCAGATT	10643
Sbjct	10550	10609
Query	10644	GGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTGAGGGCCCAA	10703
Sbjct	10610	10669
Query	10704	ACCGACACCAAAACCTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGTGAAAACCGG	10763
Sbjct	10670	10729
Query	10764	CAAAATCCAGAATTGCACAACAAATTGTTGGAGATTTTCCACACGATAGCCCAACCCACC	10823
Sbjct	10730	10789
Query	10824	CTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGGTAAATAGAAAG	10883
Sbjct	10790	10849
Query	10884	GGGGCAGCAGGCTTCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTGAGAAAAGCAC	10943
Sbjct	10850	10909
Query	10944	CTGGTAGAACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATATTATGAAACT	11003
Sbjct	10910	10969
Query	11004	GCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGGGACCTGGTG	11063
Sbjct	10970	11029

Query	11064	GTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTAGCCATCACT	11123
Sbjct	11030	11089
Query	11124	AAGGTCATGTATAACTGGGTGAAACAGCAGCCCCTTGTGATTCCAGGATATGAAGGAAAG	11183
Sbjct	11090	11149
Query	11184	ACCCCTTGTTCACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTCAATGAGCCA	11243
Sbjct	11150	11209
Query	11244	GTGGCCGTAAGTTTTGACACCAAAGCCTGGGACACTCAAGTGAAGTATAGGATCTGCAA	11303
Sbjct	11210	11269
Query	11304	CTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAGTTCATTGACACC	11363
Sbjct	11270	11329
Query	11364	ATCACCGACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTATATATAAGA	11423
Sbjct	11330	11389
Query	11424	AATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATGTTAAATGTC	11483
Sbjct	11390	11449
Query	11484	CTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGTTTCAACAGG	11543
Sbjct	11450	11509
Query	11544	GTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAAGGGTTAGGG	11603
Sbjct	11510	11569
Query	11604	CTGAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCTCAGAAGATA	11663
Sbjct	11570	11629
Query	11664	ACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTCTGTTCTCAT	11723
Sbjct	11630	11689
Query	11724	ACCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGAGACACC	11783
Sbjct	11690	11749
Query	11784	GCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGTACCACA	11843
Sbjct	11750	11809
Query	11844	GCATATGAAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCCTGGAACCCGCTTGTT	11903
Sbjct	11810	11869
Query	11904	AGGAGGATTTGCCTGTTGGTCCTTTCGCAACAGCCAGAGACAGACCCATCAAACATGCC	11963
Sbjct	11870	11929
Query	11964	ACTTATTATTACAAAGGTGATCCAATAGGGGCCATATAAGATGTAATAGGTCGGAATCTA	12023
Sbjct	11930	11989
Query	12024	AGTGAAGTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTGTCCACG	12083
Sbjct	11990	12049
Query	12084	TTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTCAGGACTGTGTTGCCATTGGG	12143
Sbjct	12050	12109
Query	12144	AAAGAAGAGGGCAACTGGCTAGTTAAGCCCGACAGGCTGATATCCAGCAAACTGGCCAC	12203
Sbjct	12110	12169
Query	12204	TTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACTGCAGCTA	12263
Sbjct	12170	12229
Query	12264	AGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTTAGGTCCCATA	12322
Sbjct	12230G.....	12289

Query	12323	GTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGTCAGCAGC	12382
Sbjct	12290	12349
Query	12383	TGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATATAAATATA	12442
Sbjct	12350	12409
Query	12443	GTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACAGTAGTCA	12502
Sbjct	12410	12469
Query	12503	AGATTATCTACCTCAAGATAACACTACATTTAATGCACACAGCACTTTAGCTGTATGAGG	12562
Sbjct	12470	12529
Query	12563	ATACGCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAG	12606
Sbjct	12530	12573

Score = 1284 bits (695), Expect = 0.0
Identities = 695/695 (100%), Gaps = 0/695 (0%)
Strand=Plus/Plus

Query	1	GTATACGAGAATTAGAAAAGGCACTCGTATACGTATTGGGCAATTAAAAATAATAATTAG	60
Sbjct	1	60
Query	61	GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG	120
Sbjct	61	120
Query	121	GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA	180
Sbjct	121	180
Query	181	GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG	240
Sbjct	181	240
Query	241	ACGAGGGCATGCCCAAAGCACATCTTAACCTGAGCGGGGGTCGCCCAGGTAAAAGCAGTT	300
Sbjct	241	300
Query	301	TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCACTGTATTGCTAC	360
Sbjct	301	360
Query	361	TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAAC'TTTTATACAAAAC	420
Sbjct	361	420
Query	421	ATACAAACAAAAACCCGTCGGGGTGGAGGAACCTGTTTATGATCAGGCAGGTGATCCCTT	480
Sbjct	421	480
Query	481	ATTTGGTGAAAGGGGAGCAGTCCACCCTCAATCGACGCTAAAGCTCCACACAAGAGAGG	540
Sbjct	481	540
Query	541	GGAACGCGATGTTCCAACCAACTTGGCATCCTTACCAAAAAGAGGTGACTGCAGGTCGGG	600
Sbjct	541	600
Query	601	TAATAGCAGAGGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGA	660
Sbjct	601	660
Query	661	CTATAAAGGTCCCGTCTATCACAGGGCCCCGCTGG	695
Sbjct	661	695

>  [gi|7960753|emb|AJ133738.1|BVI133738](#)  Bovine viral diarrhea virus complete RNA g
Length=12578

Score = 2.132e+04 bits (11546), Expect = 0.0
Identities = 11660/11690 (99%), Gaps = 8/11690 (0%)
Strand=Plus/Plus

Query	929	TCAGACACGAAAGAAGAGGGAGCAACAAAAAGAAAACACAGAAACCCGACAGACTAGAA	988
Sbjct	890	949
Query	989	AGGGGGAAAATGAAAATAGTGCCCAAAGAATCTGAAAAGACAGCAAACTAAACCTCCG	1048
Sbjct	950	1009
Query	1049	GATGCTACAATAGTGGTGGGAAGGAGTCAAATACCAGGTGAGGAAGAAGGGAAAAACCAAG	1108
Sbjct	1010	1069
Query	1109	AGTAAAAACACTCAGGACGGCTTGTACCATAACAAAAACAAACCTCAGGAATCACGCAAG	1168
Sbjct	1070	1129
Query	1169	AAACTGGAAAAAGCATTGTTGGCGTGGGCAATAATAGCTATAGTTTTGTTTCAAGTTACA	1228
Sbjct	1130	1189
Query	1229	ATGGGAGAAAACATAACACAGTGGAACCTACAAGATAATGGGACGGAAGGGATACAACGG	1288
Sbjct	1190	1249
Query	1289	GCAATGTTCCAAAGGGGTGTGAATAGAAGTTTACATGGAATCTGGCCAGAGAAAATCTGT	1348
Sbjct	1250	1309
Query	1349	ACTGGCGTCCCTTCCCATCTAGCCACCGATATAGAACTAAAACAATTTCATGGTATGATG	1408
Sbjct	1310 T	1369
Query	1409	GATGCAAGTGAGAAGACCAACTACACGTGTTGCAGACTTCAACGCCATGAGTGGAAACAAG	1468
Sbjct	1370	1429
Query	1469	CATGGTTGGTGCAACTGGTACAATATTGAACCCTGGATTCTAGTCATGAATAGAACCCAA	1528
Sbjct	1430	1489
Query	1529	GCCAATCTCACTGAGGGACAACCACCAAGGGAGTGCGCAGTCACTTGTAGGTATGATAGG	1588
Sbjct	1490	1549
Query	1589	GCTAGTGACTTAAACGTGGTAACACAAGCTAGAGATAGCCCCACACCCTTAACAGGTTGC	1648
Sbjct	1550	1609
Query	1649	AAGAAAGGAAAGAACTTCTCCTTTGCAGGCATATTGATGCGGGGCCCTGCAACTTTGAA	1708
Sbjct	1610	1669
Query	1709	ATAGCTGCAAGTGATGTATTATTCAAAGAACATGAACGCATTAGTATGTTCCAGGATACT	1768
Sbjct	1670	1729
Query	1769	ACTCTTTACCTTGTTGACGGGTTGACCAACTCCTTAGAAGGTGCCAGACAAGGAACCGCT	1828
Sbjct	1730	1789
Query	1829	AAACTGACAACCTGGTTAGGCAAGCAGCTCGGGATACTAGGAAAAAGTTGGAAAACAAG	1888
Sbjct	1790	1849
Query	1889	AGTAAGACGTGGTTTTGGAGCATACGCTGCTTCCCCTTACTGTGATGTGCGATCGCAAAATT	1948
Sbjct	1850	1909
Query	1949	GGCTACATATGGTATACAAAAAATTGCACCCCTGCCTGCTTACCCAAGAACACAAAAATT	2008
Sbjct	1910	1969
Query	2009	GTCGGCCCTGGGAAATTTGACACCAATGCAGAGGACGGCA-GATATTACATGAGATGGGG	2067
Sbjct	1970 A	2029
Query	2068	GGTCACTTGTCGGAGGTACTACTACTTTCTTTAGTGGTGCTGTCCGACTTCGCACCGGAA	2127
Sbjct	2030	2089
Query	2128	ACAGCTAGTGTAATGTACCTAATCCTACATTTTCCATCCCACAAAGTCACGTTGATGTA	2187
Sbjct	2090	2149

Query	2188	ATGGATTGTGATAAGACCCAGTTGAACCTCACAGTGGAGCTGACAACAGCTGAAGTAATA	2247
Sbjct	2150T.....	2209
Query	2248	CCAGGGTCGGTCTGGAATCTAGGCAAATATGTATGTATAAGACCAAATTGGTGGCCTTAT	2307
Sbjct	2210	..T..A..A.....C.....GG.....	2269
Query	2308	GAGACAACCTGTAGTGTGGCATTGGAAGAGGTGAGCCAGGTGGTGAAGTTAGTGTGAGG	2367
Sbjct	2270G.....	2329
Query	2368	GCACTCAGAGATTTAACACGCATTTGGAACGCTGCAACAACCTACTGCTTTTTTAGTATGC	2427
Sbjct	2330G.....C...A.....	2389
Query	2428	CTTGTTAAGATAGTCAGGGGCCAGATGGTACAGGGCATTCTGTGGCTACTATTGATAACA	2487
Sbjct	2390C.....	2449
Query	2488	GGGGTACAAGGGCACTTGGATTGCAAACCTGAATTCTCGTATGCCATAGCAAAGGACGAA	2547
Sbjct	2450	2509
Query	2548	AGAATTGGTCAACTGGGGGCTGAAGGCCTTACCACCCTTGAAGGAATACTCACCTGGA	2607
Sbjct	2510	2569
Query	2608	ATGAAGCTGGAAGACACAATGGTCATTGCTTGGTGCGAAGATGGGAAGTTAATGTACCTC	2667
Sbjct	2570	2629
Query	2668	CAAAGATGCACGAGAGAAACCAGATATCTCGCAATCTGCATACAAGAGCCTTGCCGACC	2727
Sbjct	2630	2689
Query	2728	AGTGTGGTATTCAAAAACTCTTTGATGGGCGAAAGCAAGAGGATGTAGTCGAAATGAAC	2787
Sbjct	2690	2749
Query	2788	GACAACCTTTGAATTTGGACTCTGCCCATGTGATGCCAAACCCATAGTAAGAGGGAAGTTC	2847
Sbjct	2750	2809
Query	2848	AATACAACGCTGCTGAACGGACCGGCCTTCCAGATGGTATGCCCCATAGGATGGACAGGG	2907
Sbjct	2810	2869
Query	2908	ACTGTAAGCTGTACGTCATTCAATATGGACACCTTAGCCACAACCTGTGGTACGGACATAT	2967
Sbjct	2870	2929
Query	2968	AGAAGGTCTAAACCATTCCCTCATAGGCAAGGCTGTATCACCCAAAAGAATCTGGGGGAG	3027
Sbjct	2930	2989
Query	3028	GATCTCCATAACTGCATCCTTGGAGGAAATTGGACTTGTGTGCCTGGAGACCAACTACTA	3087
Sbjct	2990	3049
Query	3088	TACAAAGGGGGCTCTATTGAATCTTGCAAGTGGTGTGGCTATCAATTTAAAGAGAGTGAG	3147
Sbjct	3050	3109
Query	3148	GGACTACCACACTACCCCATTTGGCAAGTGTAATTTGGAGAACGAGACTGGTTACAGGCTA	3207
Sbjct	3110	3169
Query	3208	GTAGACAGTACCTCTTGCAATAGAGAAGGTGTGGCCATAGTACCACAAGGGACATTAAAG	3267
Sbjct	3170	3229
Query	3268	TGCAAGATAGGAAAAACAACCTGTACAGGTCATAGCTATGGATACCAAACCTCGGACCTATG	3327
Sbjct	3230	3289
Query	3328	CCTTGACAGACCATATGAAATCATATCAAGTGAGGGGCCTGTAGAAAAGACAGCGTGTACT	3387
Sbjct	3290	3349
Query	3388	TTCAACTACACTAAGACATTAATAAATAAGTATTTGAGCCCAGAGACAGCTACTTTTCAG	3447
Sbjct	3350	3409

Query	3448	CAATACATGCTAAAAGGAGAGTATCAATACTGGTTTGACCTGGAGGTGACTGACCATCAC	3507
Sbjct	3410	3469
Query	3508	CGGGATTACTTCGCTGAGTCCATATTAGTGGTGGTAGTAGCCCTCTTGGGTGGCAGATAT	3567
Sbjct	3470	3529
Query	3568	GTACTTTGGTTACTGGTTACATACATGGTCTTATCAGAACAGAAGGCCTTAGGGATTTCAG	3627
Sbjct	3530	3589
Query	3628	TATGGATCAGGGGAAGTGGTGATGATGGGCAACTTGCTAACCATAACAATATTGAAGTG	3687
Sbjct	3590	3649
Query	3688	GTGACATACTTCTTGCTGCTGTACCTACTGCTGAGGGAGGAGAGCGTAAAGAAGTGGGTC	3747
Sbjct	3650	3709
Query	3748	TTACTCTTATACCACATCTTAGTGGTACACCCAATCAAATCTGTAATTGTGATCCTACTG	3807
Sbjct	3710	3769
Query	3808	ATGATTGGGGATGTGGTAAAGGCCGATTGAGGGGGCCAAGAGTACTTGGGGAAAATAGAC	3867
Sbjct	3770	3829
Query	3868	CTCTGTTTTACAACAGTAGTACTAATCGTCATAGGTTAATCATAGCCAGGCGTGACCCA	3927
Sbjct	3830	3889
Query	3928	ACTATAGTGCCACTGGTAACAATAATGGCAGCACTGAGGGTCACTGAACTGACCCACCAG	3987
Sbjct	3890	3949
Query	3988	CCTGGAGTTGACATCGCTGTGGCGGTCATGACTATAACCCTACTGATGGTTAGCTATGTG	4047
Sbjct	3950	4009
Query	4048	ACAGATTATTTTAGATATAAAAAATGGTTACAGTGCATTCTCAGCCTGG-ATCTGGGGTG	4106
Sbjct	4010T.....	4069
Query	4107	TTCTTGATAAGAAGCCTAATATACCTAGGTAGAATCGAGATGCCAGAGGTAACATCCCA	4166
Sbjct	4070	4129
Query	4167	AACTGGAGACCACTAACTTTAATACTATTATATTTGATCTCAACAACAATTGTAACGAGG	4226
Sbjct	4130	4189
Query	4227	TGGAAGGTTGACGTGGCTGGCCTATTGTTGCAATGTGTGCCTATCTTATTGCTGGTCACA	4286
Sbjct	4190	4249
Query	4287	ACCTTGTTGGGCCGACTTCTTAACCCTAATACTGATCCTGCCTACCTATGAATTGGTTAAA	4346
Sbjct	4250	4309
Query	4347	TTATACTATCTGAAAACGTGTTAGGACTGATATAGAAAGAAGTTGGCTAGGGGGGATAGAC	4406
Sbjct	4310	4369
Query	4407	TATACAAGAGTTGACTCCATCTACGACGTTGATGAGAGTGGAGAGGGCGTATATCTTTTT	4466
Sbjct	4370	4429
Query	4467	CCATCAAGGCAGAAAGCACAGGGGAATTTTTCTATACTCTTGCCCCCTTATCAAAGCAACA	4526
Sbjct	4430	4489
Query	4527	CTGATAAGTTGCGTCAGCAGTAAATGGCAGCTAATATACATGAGTTACTTAACTTTGGAC	4586
Sbjct	4490	4549
Query	4587	TTTATGTACTACATGCACAGGAAAGTTATAGAAGAGATCTCAGGAGGTACCAACATAATA	4646
Sbjct	4550	4609
Query	4647	TCCAGGTTAGTGGCAGCACTCATAGAGCTGAACTGGTCCATGGAAGAAGAGGAGAGCAAA	4706
Sbjct	4610	4669

Query	4707	GGCTTAAAGAAGTTTTATCTATTGTCTGGAAGGTTGAGAAACCTAATAATAAACATAAG	4766
Sbjct	4670	4729
Query	4767	GTAAGGAATGAGACCGTGGCTTCTTGGTACGGGGAGGAGGAAGTCTACGGTATGCCAAAG	4826
Sbjct	4730	4789
Query	4827	ATCATGACTATAATCAAGGCCAGTACACTGAGTAAGAGCAGGCACTGCATAATATGCACT	4886
Sbjct	4790	4849
Query	4887	GTATGTGAGGGCCGAGAGTGGAAAGGTGGCACCTGCCCAAATGTGGACGCCATGGGAAG	4946
Sbjct	4850	4909
Query	4947	CCGATAACGTGTGGGATGTCGCTAGCAGATTTTGAAGAAAGACACTATAAAAGAATCTTT	5006
Sbjct	4910	4969
Query	5007	ATAAGGGAAGGCAACTTTGAGGGTATGTGCAGCCGATGCCAGGGAAGCATAGGAGGTTT	5066
Sbjct	4970	5029
Query	5067	GAAATGGACCGGGAACCTAAGAGTGCCAGATACTGTGCTGAGTGTAAATAGGCTGCATCCT	5126
Sbjct	5030	5089
Query	5127	GCTGAGGAAGGTGACTTTTGGGCAGAGTCGAGCATGTTGGGCCCTCAAATCACCTACTTT	5186
Sbjct	5090	5149
Query	5187	GCGCTGATGGATGGAAAGGTGTATGATATCACAGAGTGGGCTGGATGCCAGCGTGTGGGA	5246
Sbjct	5150	5209
Query	5247	ATCTCCCCAGATACCCACAGAGTCCCTTGTACATCTCATTTGGTTTACGGATGCCTTTC	5306
Sbjct	5210	5269
Query	5307	AGGCAGGAATACAATGGCTTTGTACAATATACCGCTAGGGGGCAACTATTTCTGAGAAAC	5366
Sbjct	5270	5329
Query	5367	TTGCCCCGTACTGGCAACTAAAGTAAAAATGCTCATGGTAGGCAACCTTGGAGAAGAAATT	5426
Sbjct	5330	5389
Query	5427	GGTAATCTGGAACATCTTGGGTGGATCCTAAGGGGGCCTGCCGTGTGTAAGAAGATCACA	5486
Sbjct	5390	5449
Query	5487	GAGCACGAAAAATGCCACATTAATATACTGGATAAACTAACCGCATTTTTTCGGGATCATG	5546
Sbjct	5450	5509
Query	5547	CCAAGGGGGACTACACCCAGAGCCCCGGTGAGGTTCCCTACGAGCTTACTAAAAGTGAGG	5606
Sbjct	5510	5569
Query	5607	AGGGGTCTGGAGACTGGCTGGGCTTACACACACCAAGGCGGGATAAGTTTCAGTCGACCAT	5666
Sbjct	5570	5629
Query	5667	GTAACCGCCGGAAAAGATCTACTGGTCTGTGACAGCATGGGACGAACTAGAGTGGTTTGC	5726
Sbjct	5630	5689
Query	5727	CAAAGCAACAACAGGTTGACCGATGAGACAGAGTATGGCGTCAAGACTGACTCAGGGTGC	5786
Sbjct	5690	5749
Query	5787	CCAGACGGTGCCAGATGTTATGTGTTAAATCCAGAGGCCGTTAACATATCAGGATCCAAA	5846
Sbjct	5750	5809
Query	5847	GGGGCAGTCGTTTCCCTCCAAAAGACAGGTGGAGAATTACGTTGTGTACCGCATCAGGC	5906
Sbjct	5810	5869
Query	5907	ACACCGGCTTTCTTCGACCTAAAAAACTTGAAAGGATGGTCAGGCTTGCCTATATTTGAA	5966
Sbjct	5870	5929

Query	5967	GCCTCCAGCGGGAGGGTGGTTGGCAGAGTCAAAGTAGGGAAGAATGAAGAGTCTAAACCT	6026
Sbjct	5930	5989
Query	6027	ACAAAAATAATGAGTGGAAATCCAGACCGTCTCAAAAAACACAGCAGACCTGACCGAGATG	6086
Sbjct	5990	6049
Query	6087	GTCAAGAAGATAACCAGCATGAACAGGGGAGACTTCAAGCAGATTACTTTGGCAACAGGG	6146
Sbjct	6050	6109
Query	6147	-CAGGCAAACCACAGAACTCCCAAAAGCAGTTATAGAGGAGATAGGAAGACACAAGAGA	6205
Sbjct	6110	G.....	6169
Query	6206	GTATTAGTTCTTATACCATTAAGGGCAGCGGCAGAGTCAGTCTACCAGTATATGAGATTG	6265
Sbjct	6170	6229
Query	6266	AAACACCCAAGCATCTCTTTTAACCTAAGGATAGGGGACATGAAAGAGGGGGACATGGCA	6325
Sbjct	6230	6289
Query	6326	ACCGGGATAACCTATGCATCATACGGGTACTTCTGCCAAATGCCTCAACCAAGCTCAGA	6385
Sbjct	6290	6349
Query	6386	GCTGCTATGGTAGAATACTCATACATATTCTTAGATGAATACCATTGTGCCACTCCTGAA	6445
Sbjct	6350	6409
Query	6446	CAACTGGCAATTATCGGGAAGATCCACAGATTTTCAGAGAGTATAAGGGTTGTCGCCATG	6505
Sbjct	6410	6469
Query	6506	ACTGCCACGCCAGCAGGGTCGGTGACCACAACAGGTCAAAGCACCCAATAGAGGAATTC	6565
Sbjct	6470	6529
Query	6566	ATAGCCCCCGAGGTAATGAAAGGGGAGGATCTTGGTAGTCAGTTCCTTGATATAGCAGGG	6625
Sbjct	6530	6589
Query	6626	TTAAAAATACCAGTGGATGAGATGAAAGGCAATATGTTGGTTTTTGTACCAACGAGAAAC	6685
Sbjct	6590	6649
Query	6686	ATGGCAGTAGAGGTAGCAAAGAAGCTAAAAGCTAAGGGCTATAACTCTGGATACTATTAC	6745
Sbjct	6650	6709
Query	6746	AGTGGAGAGGATCCAGCCAATCTGAGAGTTGTGACATCACAATCCCCCTATGTAATCGTG	6805
Sbjct	6710	6769
Query	6806	GCTACAAATGCTATTGAATCAGGAGTGACACTACCAGATTTGGACACGGTTATAGACACG	6865
Sbjct	6770	6829
Query	6866	GGGTTGAAATGTGAAAAGAGGGTGAGGGTATCATCAAAGATAACCTTCATCGTAACAGGC	6925
Sbjct	6830	6889
Query	6926	CTTAAGAGGATGGCCGTGACTGTGGGTGAGCAGGCGCAGCGTAGGGGCAGAGTAGGTAGA	6985
Sbjct	6890	6949
Query	6986	GTGAAACCCGGGAGGTATTATAGGAGCCAGGAAACAGCAACAGGGTCAAAGGACTACCAC	7045
Sbjct	6950T....	7009
Query	7046	TATGACCTCTTGCAGGCACAAAGATACGGGATTGAGGATGGAATCAACGTGACGAAATCC	7105
Sbjct	7010	7069
Query	7106	TTTAGGGAGATGAATTACGATTGGAGCCTATACGAGGAGGACAGCCTACTAATAACCCAG	7165
Sbjct	7070	7129
Query	7166	CTGGAAATACTAAATAATCTACTCATCTCAGAAGACTTGCCAGCCGCTGTTAAGAACATA	7225
Sbjct	7130	7189

Query	7226	ATGGCCAGGACTGATCACCCAGAGCCAATCCAACCTTGCATACAACAGCTATGAAGTCCAG	7285
Sbjct	7190	7249
Query	7286	GTCCCGGTCCTATTCCCAAAAATAAGGAATGGAGAAGTCACAGACACCTACGAAAATTAC	7345
Sbjct	7250G.....	7309
Query	7346	TCGTTTCTAAATGCCAGAAAGTTAGGGGAGGATGTGCCCGTGTATATCTACGCTACTGAA	7405
Sbjct	7310	7369
Query	7406	GATGAGGATCTGGCAGTTGACCTCTTAGGGCTAGACTGGCCTGATCCTGGGAACCAGCAG	7465
Sbjct	7370	7429
Query	7466	GTAGTGGAGACTGGTAAAGCACTGAAGCAAGTGACCGGGTTGTCTCGGCTGAAAATGCC	7525
Sbjct	7430	7489
Query	7526	CTACTAGTGGCTTTATTTGGGTATGTGGGTACCAGGCTCTCTCAAAGAGGCATGTCCCA	7585
Sbjct	7490	7549
Query	7586	ATGATAACAGACATATATACCATCGAGGACCAGAGACTAGAAGACACCACCCACCTCCAG	7645
Sbjct	7550	7609
Query	7646	TATGCACCCAACGCCATAAAAACCGATGGGACAGAGACTGAACTGAAAGAACTGGCGTCG	7705
Sbjct	7610	7669
Query	7706	GGTGACGTGGAAAAAATCATGGGAGCCATTTAGATTATGCAGCTGGGGGACTGGAGTTT	7765
Sbjct	7670	7729
Query	7766	GTTAAATCCCAAGCAGAAAAGATAAAAACAGCTCCTTTGTTTAAAGAAAACGCAGAAGCC	7825
Sbjct	7730	7789
Query	7826	GCAAAAGGGTATGTCCAAAATTCATTGACTCATTAATTGAAAATAAAGAAGAAATAATC	7885
Sbjct	7790	7849
Query	7886	AGATATGGTTTGTGGGGAACACACAGCACTATACAAAAGCATAGCTGCAAGACTGGGG	7945
Sbjct	7850	7909
Query	7946	CATGAAACAGCGTTTGCCACACTAGTGTTAAAGTGGCTAGCTTTTGGAGGGGAATCAGTG	8005
Sbjct	7910	7969
Query	8006	TCAGACCACGTCAAGCAGGCGGCAGTTGATTTAGTGGTCTATTATGTGATGAATAAGCCT	8065
Sbjct	7970	8029
Query	8066	TCCTTCCCAGGTGACTCCGAGACACAGCAAGAAGGGAGGCGATTTCGTCGCAAGCCTGTTT	8125
Sbjct	8030	8089
Query	8126	ATCTCCGCACTGGCAACCTACACATACAAAACCTTGAATTACCACAATCTCTCTAAAGTG	8185
Sbjct	8090	8149
Query	8186	GTGGAAC-AGCCCTGGCTTACCTCCCCTATGCTACCAGCGCATTAAAAATGTTACCCCCA	8244
Sbjct	8150C.....	8209
Query	8245	ACGCGGCTGGAGAGCGTGGTGATACTGAGCACCACGATATATAAAACATACCTCTCTATA	8304
Sbjct	8210	8269
Query	8305	AGGAAGGGGAAGAGTGATGGATTGCTGGGTACGGGGATAAGTGCAGCCATGGAAATCCTG	8364
Sbjct	8270	8329
Query	8365	TCACAAAACCCAGTATCGGTAGGTATATCTGTGATGTTGGGGGTAGGGGCAATCGCTGCG	8424
Sbjct	8330	8389
Query	8425	CACAACGCTATTGAGTCCAGTGAACAGAAAAGGACCCTACTTATGAAGGTGTTTGTAAG	8484
Sbjct	8390	8449

Query	8485	AACTTCTTGGATCAGGCTGCAACAGATGAGCTGGTAAAAGAAAACCCAGAAAAAATTATA	8544
Sbjct	8450	8509
Query	8545	ATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCCTGAGACTAATATACCACCTG	8604
Sbjct	8510	8569
Query	8605	TATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAACCTATCTGAGAGGACAGCAGGCAGA	8664
Sbjct	8570	8629
Query	8665	AACTTATTACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGACTCACAAAGGG	8724
Sbjct	8630	8689
Query	8725	AAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTACACAAGCAA	8784
Sbjct	8690	8749
Query	8785	ATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCTGCACCCTTTAGTTGTGAC	8844
Sbjct	8750	8809
Query	8845	TGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAACCTATTTGAGGGTAGAAACC	8904
Sbjct	8810	8869
Query	8905	AGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAACCTACCAAA	8964
Sbjct	8870	8929
Query	8965	GTGGAGGAGAGCGGGCCTTTCCTATGTAGAAACAGACCTGGTAGGGGACCAGTCAACTAC	9024
Sbjct	8930	8989
Query	9025	AGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCAAAGTTGGAA	9084
Sbjct	8990	9049
Query	9085	GGACAGGTAGAGCACTACTACAAAGGGGTACAGCAAAAATTGACTACAGTAAAGGAAAA	9144
Sbjct	9050	9109
Query	9145	ATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGGTTAGCTAAG	9204
Sbjct	9110	9169
Query	9205	AGATATACTGGGGTCGGGTTCAATGGTGCATACTTAGGTGACGAGCCCAATCACCGTGCT	9264
Sbjct	9170	9229
Query	9265	CTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTAAAAATGAAG	9324
Sbjct	9230	9289
Query	9325	AAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTCATCGAACTA	9384
Sbjct	9290	9349
Query	9385	GTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACCACATGGCTA	9444
Sbjct	9350	9409
Query	9445	GCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGAGAGAGAGTA	9504
Sbjct	9410	9469
Query	9505	ATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGACACGTCAGAG	9564
Sbjct	9470	9529
Query	9565	GTTGGGATCACAATAATTGGAAGGGAAACCCTGATGACAACGGGAGTGACACCTGTCTTG	9624
Sbjct	9530	9589
Query	9625	GAAAAAGTAGAGCCTGACGCCAGCGACAACCAAAACTCGGTGAAGATCGGGTTGGATGAG	9684
Sbjct	9590	9649
Query	9685	GGTAATTACCCAGGGCCTGGAATACAGACACATACACTAACAGAAGAAATACACAACAGG	9744
Sbjct	9650	9709

Query	9745	GATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATTCATATCAAATAGGGCAAAG	9804
Sbjct	9710	9769
Query	9805	ACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCCAGGGAAATACGAGACTTGATG	9864
Sbjct	9770	9829
Query	9865	GCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTCGACCCTGAGCTGTCTGAAATG	9924
Sbjct	9830	9889
Query	9925	GTCGATTTCAAGGGGACTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGTCTCGGGCAA	9984
Sbjct	9890	9949
Query	9985	CCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAGAAAAAGAT	10044
Sbjct	9950	10009
Query	10045	GTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTGGCCTTAAAA	10104
Sbjct	10010	10069
Query	10105	AATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCTAAAGCACTT	10164
Sbjct	10070G.....	10129
Query	10165	GGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTATGCCATGAAG	10224
Sbjct	10130	10189
Query	10225	CTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCACTGTTTGAG	10283
Sbjct	10190T.C.....	10249
Query	10284	GAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATGGCATCAGCT	10343
Sbjct	10250	10309
Query	10344	TACCAATTGGCACAGGGTAACTGGGAGCCCTCGGTTGCGGGGTGCACCTAGGTACAATA	10403
Sbjct	10310	10369
Query	10404	CCAGCCAGAAGGGTGAAGATACCCCATATGAAGCTTACCTGAAGTTGAAAGATTTCATa	10463
Sbjct	10370	10429
Query	10464	gaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCACAAACAATGG	10523
Sbjct	10430	10489
Query	10524	ATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTCAACCCAGGG	10583
Sbjct	10490T...	10549
Query	10584	AAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAACCACCAGATT	10643
Sbjct	10550	10609
Query	10644	GGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTGAGGGCCCAA	10703
Sbjct	10610	10669
Query	10704	ACCGACACCAAAACCTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGTAAAACCGG	10763
Sbjct	10670	10729
Query	10764	CAAAATCCAGAATTGCACAACAAATTGTTGGAGATTTCCACACGATAGCCCAACCCACC	10823
Sbjct	10730	10789
Query	10824	CTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGTAAATAGAAAG	10883
Sbjct	10790A.....	10849
Query	10884	GGGGCAGCAGGCTTCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTGAGAAAAGCAC	10943
Sbjct	10850	10909
Query	10944	CTGGTAGAACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATATTATGAACT	11003
Sbjct	10910	10969

Query	11004	GCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGGGACCTGGTG	11063
Sbjct	10970	11029
Query	11064	GTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTAGCCATCACT	11123
Sbjct	11030	11089
Query	11124	AAGGTCATGTATAACTGGGTGAAACAGCAGCCCGTTGTGATTCCAGGATATGAAGGAAAG	11183
Sbjct	11090	11149
Query	11184	ACCCCTTGTTC AACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTCAATGAGCCA	11243
Sbjct	11150	11209
Query	11244	GTGGCCGTAAGTTTTGACACCAAAGCCTGGGACACTCAAGTGACTAGTAAGGATCTGCAA	11303
Sbjct	11210	11269
Query	11304	CTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAAGTTCATTGACACC	11363
Sbjct	11270	11329
Query	11364	ATCACC GACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTATATATAAGA	11423
Sbjct	11330	11389
Query	11424	AATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATGTTAAATGTC	11483
Sbjct	11390	11449
Query	11484	CTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGTTTCAACAGG	11543
Sbjct	11450C.....	11509
Query	11544	GTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAGGGTTAGGG	11603
Sbjct	11510	11569
Query	11604	CTGAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCTCAGAAGATA	11663
Sbjct	11570	11629
Query	11664	ACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTCTGTTCTCAT	11723
Sbjct	11630	11689
Query	11724	ACCC CAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGAGACACC	11783
Sbjct	11690	11749
Query	11784	GCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGTACCACA	11843
Sbjct	11750T	11809
Query	11844	GCATATGAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCTTGGAAACCCGCTTGTT	11903
Sbjct	11810	11869
Query	11904	AGGAGGATTTGCCTGTTGGTCCTTTCGCAACAGCCAGAGACAGACCCATCAAAACATGCC	11963
Sbjct	11870	11929
Query	11964	ACTTATTATTACAAAGGTGATCCAATAGGGGCCATATAAAGATGTAATAGGTGCGAATCTA	12023
Sbjct	11930	11989
Query	12024	AGTGAAC TGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTGTCCACG	12083
Sbjct	11990	12049
Query	12084	TTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATT CAGGACTGTGTTGCCATTGGG	12143
Sbjct	12050A.....	12109
Query	12144	AAAGAAGAGGGCAACTGGCTAGTTAA-GCCCGACAGGCTGATATCCAGCAAAACTGGCCA	12202
Sbjct	12110C.....	12168
Query	12203	CTTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACTGCAGCT	12262
Sbjct	12169	12228

Query	12263	AAGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTTAGGTCCCAT	12321
Sbjct	12229G.....	12288
Query	12322	AGTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGTCAGCAG	12381
Sbjct	12289	12348
Query	12382	CTGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATATAAATAT	12441
Sbjct	12349	12408
Query	12442	AGTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACAGTAGTC	12501
Sbjct	12409	12468
Query	12502	AAGATTATCTACCTCAAGATAACACTACATTTAATGCACACAGCACTTTAGCTGTATGAG	12561
Sbjct	12469	12528
Query	12562	GATACGCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAGCCCCC	12611
Sbjct	12529	12578

Score = 1284 bits (695), Expect = 0.0
Identities = 695/695 (100%), Gaps = 0/695 (0%)
Strand=Plus/Plus

Query	1	GTATACGAGAATTAGAAAAGGCACCTCGTATACGTATTGGGCAATTAAAAATAATAATTAG	60
Sbjct	1	60
Query	61	GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG	120
Sbjct	61	120
Query	121	GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA	180
Sbjct	121	180
Query	181	GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG	240
Sbjct	181	240
Query	241	ACGAGGGCATGCCCAAAGCACATCTTAACCTGAGCGGGGGTCGCCCAGGTAAAAGCAGTT	300
Sbjct	241	300
Query	301	TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCACTGTATTGCTAC	360
Sbjct	301	360
Query	361	TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAACTTTTATACAAAAC	420
Sbjct	361	420
Query	421	ATACAAACAAAACCCGTCGGGGTGGAGGAACCTGTTTATGATCAGGCAGGTGATCCCTT	480
Sbjct	421	480
Query	481	ATTTGGTGAAAGGGGAGCAGTCCACCCTCAATCGACGCTAAAGCTCCACACAAGAGAGG	540
Sbjct	481	540
Query	541	GGAACGCGATGTTCCAACCAACTTGGCATCCTTACCAAAAAGAGGTGACTGCAGGTCGGG	600
Sbjct	541	600
Query	601	TAATAGCAGAGGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGA	660
Sbjct	601	660
Query	661	CTATAAAGGTCCCGTCTATCACAGGGCCCCGCTGG	695
Sbjct	661	695

> [gi|9049956|gb|AF268278.1|AF268278](#) **D** Pestivirus type 1, complete genome
Length=12734

Score = 2.131e+04 bits (11537), Expect = 0.0
 Identities = 11657/11691 (99%), Gaps = 8/11691 (0%)
 Strand=Plus/Plus

Query	928	TTCAGACACGAAAGAAGAGGGAGCAACAAAAAGAAAACACAGAAACCCGACAGACTAGA	987
Sbjct	1045	1104
Query	988	AAGGGGGAAAATGAAAATAGTGCCCAAAGAATCTGAAAAAGACAGCAAACTAAACCTCC	1047
Sbjct	1105C..	1164
Query	1048	GGATGCTACAATAGTGGTGGGAAGGAGTCAAATACCAGGTGAGGAAGAAGGGAAAAACCAA	1107
Sbjct	1165	1224
Query	1108	GAGTAAAAACACTCAGGACGGCTTGTACCATAACAAAAACAAACCTCAGGAATCACGCAA	1167
Sbjct	1225	1284
Query	1168	GAAACTGGAAAAAGCATTGTTGGCGTGGGCAATAATAGCTATAGTTTTGTTTCAAGTTAC	1227
Sbjct	1285C.....	1344
Query	1228	AATGGGAGAAAACATAACACAGTGGAACTACAAGATAATGGGACGGAAGGGATACAACG	1287
Sbjct	1345	1404
Query	1288	GGCAATGTTCCAAAGGGGTGTGAATAGAAGTTTACATGGAATCTGGCCAGAGAAAATCTG	1347
Sbjct	1405	1464
Query	1348	TACTGGCGTCCCTTCCCCTCTAGCCACCGATATAGAACTAAAAACAATTCATGGTATGAT	1407
Sbjct	1465T.....	1524
Query	1408	GGATGCAAGTGAGAAGACCAACTACACGTGTTGCAGACTTCAACGCCATGAGTGGAAACAA	1467
Sbjct	1525A.....	1584
Query	1468	GCATGGTTGGTGCAACTGGTACAATATTGAACCCTGGATTCTAGTCATGAATAGAACCCA	1527
Sbjct	1585	1644
Query	1528	AGCCAATCTCACTGAGGGACAACCACCAAGGGAGTGCGCAGTCACTTGTAGGTATGATAG	1587
Sbjct	1645	1704
Query	1588	GGCTAGTGACTTAAACGTGGTAACACAAGCTAGAGATAGCCCCACACCCTTAACAGGTTG	1647
Sbjct	1705	1764
Query	1648	CAAGAAAGGAAAGAACTTCTCCTTTGCAGGCATATTGATGCGGGGCCCCCTGCAACTTTGA	1707
Sbjct	1765	1824
Query	1708	AATAGCTGCAAGTGATGTATTATTCAAAGAACATGAACGCATTAGTATGTTCCAGGATAC	1767
Sbjct	1825	1884
Query	1768	TACTCTTTACCTTGTGACGGGTTGACCAACTCCTTAGAAGGTGCCAGACAAGGAACCGC	1827
Sbjct	1885	1944
Query	1828	TAAACTGACAACCTGGTTAGGCAAGCAGCTCGGGATACTAGGAAAAAAGTTGGAAAACAA	1887
Sbjct	1945	2004
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Sbjct	2005T.....	2064
Query	1948	TGGCTACATATGGTATACAAAAAATTGCACCCCTGCCTGCTTACCCAAGAACACAAAAAT	2007
Sbjct	2065	2124
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Sbjct	2125A.....	2184
Query	2067	GGGTCACTTGTCGGAGGTACTACTACTTTCTTTAGTGGTGTGTCGACTTCGCACCGGA	2126

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Sbjct	2245	2304
Query	2187	AATGGATTGTGATAAGACCCAGTTGAACCTCACAGTGGAGCTGACAACAGCTGAAGTAAT	2246
Sbjct	2305T.....	2364
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Sbjct	2365	...T..A..A.....C.....GG.....	2424
Query	2307	TGAGACAACCTGTAGTGTTGGCATTGGAAGAGGTGAGCCAGGTGGTGAAGTTAGTGTTGAG	2366
Sbjct	2425G.....	2484
Query	2367	GGCACTCAGAGATTTAACACGCATTTGGAACGCTGCAACAACCTACTGCTTTTTTAGTATG	2426
Sbjct	2485G.....C...A....	2544
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Sbjct	2545C.....	2604
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Sbjct	2665	2724
Query	2607	AATGAAGCTGGAAGACACAATGGTCATTGCTTGGTGCGAAGATGGGAAGTTAATGTACCT	2666
Sbjct	2725	2784
Query	2667	CCAAAGATGCACGAGAGAAACCAGATATCTCGCAATCTTGCATACAAGAGCCTTGCCGAC	2726
Sbjct	2785	2844
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Query	2787	CGACAACCTTTGAATTTGGACTCTGCCCATGTGATGCCAAACCCATAGTAAGAGGGAAGTT	2846
Sbjct	2905	2964
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Sbjct	2965	3024
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Sbjct	3025	3084
Query	2967	TAGAAGGTCTAAACCATTCCTCATAGGCAAGGCTGTATCACCCAAAAGAATCTGGGGGA	3026
Sbjct	3085	3144
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Sbjct	3145	3204
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Sbjct	3205	3264
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Sbjct	3265	3324
Query	3207	AGTAGACAGTACCTCTTGCAATAGAGAAGGTGTGGCCATAGTACCACAAGGGACATTAAA	3266
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Sbjct	3565	3624
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Query	3567	TGTACTTTGGTTACTGGTTACATACATGGTCTTATCAGAACAGAAGGCCCTTAGGGATTCA	3626
Sbjct	3685	3744
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Sbjct	3805	3864
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Sbjct	4405	4464
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Sbjct	4465	4524
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Sbjct	4525	4584
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Sbjct	4765	4824
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Sbjct	4945	5004
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Sbjct	5185	5244
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Sbjct	5245	5304
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Sbjct	5305	5364
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Sbjct	5545	5604
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Sbjct	5605	5664
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Sbjct	5665	5724
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Sbjct	5725	5784
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Query	5726	CCAAAGCAACAACAGGTTGACCGATGAGACAGAGTATGGCGTCAAGACTGACTCAGGGTG	5785
Sbjct	5845	5904
Query	5786	CCCAGACGGTGCCAGATGTTATGTGTTAAATCCAGAGGCCGTTAACATATCAGGATCCAA	5845
Sbjct	5905	5964
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Sbjct	6025	6084
Query	5966	AGCCTCCAGCGGGAGGGTGGTTGGCAGAGTCAAAGTAGGGAAGAATGAAGAGTCTAAACC	6025
Sbjct	6085	6144
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Sbjct	6145	6204
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Sbjct	6505	6564
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Sbjct	6565	6624
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Sbjct	7165	7224
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Sbjct	8845	8904
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Sbjct	10045	10104
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Sbjct	10525	10584
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Sbjct	10765	10824
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Sbjct	11065	11124
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Sbjct	11125	11184
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Sbjct	11185	11244
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Sbjct	11245	11304
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Sbjct	11305	11364
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Sbjct	11425	11484
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Sbjct	11485	11544
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Sbjct	11545	11604
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Sbjct	11605 C	11664
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Sbjct	11665	11724
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Sbjct	11725	11784
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Sbjct	11785	11844
Query	11723	TACCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGAGACAC	11782
Sbjct	11845	11904
Query	11783	CGCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGTACCAC	11842
Sbjct	11905	11964
Query	11843	AGCATATGAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCTTGGAAACCCGCTTGT	11902
Sbjct	11965	W	12024
Query	11903	TAGGAGGATTTGCCTGTTGGTCCCTTTCGCAACAGCCAGAGACAGACCCATCAAACATGC	11962
Sbjct	12025	12084
Query	11963	CACTTATTATTACAAAGGTGATCCAATAGGGGCCATAAAAGATGTAATAGGTCGGAATCT	12022
Sbjct	12085	12144
Query	12023	AAGTGAACCTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTGTCCAC	12082
Sbjct	12145	12204
Query	12083	GTTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTCAAGGACTGTGTTGCCATTGG	12142
Sbjct	12205 A	12264
Query	12143	GAAAGAAGAGGGCAACTGGCTAGTTAA-GCCCGACAGGCTGATATCCAGCAAACTGGCC	12201

Sbjct	12265C.....-	12323
Query	12202	ACTTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACTGCAGC	12261
Sbjct	12324	12383
Query	12262	TAAGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTTAGGTCCCA	12320
Sbjct	12384G.....	12443
Query	12321	TAGTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGTCAGCA	12380
Sbjct	12444	12503
Query	12381	GCTGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATATAAATA	12440
Sbjct	12504	12563
Query	12441	TAGTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACAGTAGT	12500
Sbjct	12564	12623
Query	12501	CAAGATTATCTACCTCAAGATAAACTACATTTAATGCACACAGCACTTTAGCTGTATGA	12560
Sbjct	12624	12683
Query	12561	GGATACGCCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAGCCCCC	12611
Sbjct	12684	12734

Score = 745 bits (403), Expect = 0.0
Identities = 405/406 (99%), Gaps = 0/406 (0%)
Strand=Plus/Plus

Query	1	GTATACGAGAATTAGAAAAGGCACTCGTATACGTATTGGGCAATTAAAAATAATAATTAG	60
Sbjct	1	60
Query	61	GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG	120
Sbjct	61	120
Query	121	GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA	180
Sbjct	121	180
Query	181	GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG	240
Sbjct	181	240
Query	241	ACGAGGGCATGCCCAAAGCACATCTTAACCTGAGCGGGGGTCGCCCAGGTAAAAGCAGTT	300
Sbjct	241	300
Query	301	TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCCTGTATTGCTAC	360
Sbjct	301	360
Query	361	TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAA	406
Sbjct	361A.....	406

> [gi|55724858|emb|AJ781045.1|](#) Bovine viral diarrhea virus partial PPP gene for pol
genomic RNA, strain NADL
Length=8712

Score = 1.573e+04 bits (8518), Expect = 0.0
Identities = 8666/8713 (99%), Gaps = 7/8713 (0%)
Strand=Plus/Plus

Query	3679	ATTGAAGTGGTGACATACTTCTTGCTGCTGTACCTACTGCTGAGGGAGGAGAGCGTAAAG	3738
Sbjct	1A.....	60
Query	3739	AAGTGGGTCTTACTCTTATACCACATCTTAGTGGTACACCCAATCAAATCTGTAATTGTG	3798
Sbjct	61G....C.....	120

Query	3799	ATCCTACTGATGATTGGGGATGTGGTAAAGGCCGATTAGGGGGCCAAGAGTACTTGGGG	3858
Sbjct	121	180
Query	3859	AAAATAGACCTCTGTTTTACAACAGTAGTACTAATCGTCATAGGTTTAAATCATAGCCAGG	3918
Sbjct	181	C.....	240
Query	3919	CGTGACCCAACTATAGTGCCACTGGTAACAATAATGGCAGCACTGAGGGTCACTGAACTG	3978
Sbjct	241T..	300
Query	3979	ACCCACCAGCCTGGAGTTGACATCGCTGTGGCGGTCATGACTATAACCCTACTGATGGTT	4038
Sbjct	301	360
Query	4039	AGCTATGTGACAGATTATTTTAGATATAAAAAATGGTTACAGTGCATTCTCAGCCTGG-A	4097
Sbjct	361T.	420
Query	4098	TCTGGGGTGTTCCTTGATAAGAAGCCTAATATACCTAGGTAGAATCGAGATGCCAGAGGTA	4157
Sbjct	421	480
Query	4158	ACTATCCCAAACCTGGAGACCACTAACTTTAATACTATTATATTTGATCTCAACAACAATT	4217
Sbjct	481C.....	540
Query	4218	GTAACGAGGTGGAAGGTTGACGTGGCTGGCCTATTGTTGCAATGTGTGCCTATCTTATTG	4277
Sbjct	541	600
Query	4278	CTGGTCACAACCTTGTGGGCCGACTTCTTAACCCTAATACTGATCCTGCCTACCTATGAA	4337
Sbjct	601	660
Query	4338	TTGGTTAAATTATACTATCTGAAAACGTTAGGACTGATATAGAAAGAAGTTGGCTAGGG	4397
Sbjct	661	720
Query	4398	GGGATAGACTATACAAGAGTTGACTCCATCTACGACGTTGATGAGAGTGGAGAGGGCGTA	4457
Sbjct	721	780
Query	4458	TATCTTTTTCCATCAAGGCAGAAAGCACAGGGGAATTTTTCTATACTCTTGCCCTTATC	4517
Sbjct	781TA.....	840
Query	4518	AAAGCAACACTGATAAGTTGCGTCAGCAGTAAATGGCAGCTAATATACATGAGTTACTTA	4577
Sbjct	841	900
Query	4578	ACTTTGGACTTTATGTACTACATGCACAGGAAAGTTATAGAAGAGATCTCAGGAGGTACC	4637
Sbjct	901	960
Query	4638	AACATAATATCCAGGTTAGTGGCAGCACTCATAGAGCTGAACGGTCCATGGAAGAAGAG	4697
Sbjct	961G.....	1020
Query	4698	GAGAGCAAAGGCTTAAAGAAGTTTTATCTATTGTCTGGAAGGTTGAGAAACCTAATAATA	4757
Sbjct	1021	1080
Query	4758	AAACATAAGGTAAGGAATGAGACCGTGGCTTCTTGGTACGGGGAGGAGGAAGTCTACGGT	4817
Sbjct	1081A.....C	1140
Query	4818	ATGCCAAAGATCATGACTATAATCAAGGCCAGTACACTGAGTAAGAGCAGGCACCTGCATA	4877
Sbjct	1141	1200
Query	4878	ATATGCACTGTATGTGAGGGCCGAGAGTGGAAAGGTGGCACCTGCCCAAATGTGGACGC	4937
Sbjct	1201	1260
Query	4938	CATGGGAAGCCGATAACGTGTGGGATGTCGCTAGCAGATTTTCAAGAAAGACACTATAAA	4997
Sbjct	1261T.....	1320
Query	4998	AGAATCTTTATAAGGGAAGGCAACTTTGAGGGTATGTGCAGCCGATGCCAGGGAAAGCAT	5057
Sbjct	1321	1380

Query	5058	AGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATACTGTGCTGAGTGTAATAGG	5117
Sbjct	1381C.....	1440
Query	5118	CTGCATCCTGCTGAGGAAGGTGACTTTTGGGCAGAGTCGAGCATGTTGGGCCTCAAATC	5177
Sbjct	1441A.....	1500
Query	5178	ACCTACTTTGCGCTGATGGATGGAAAGGTGTATGATATCACAGAGTGGGCTGGATGCCAG	5237
Sbjct	1501G.....	1560
Query	5238	CGTGTGGGAATCTCCCCAGATACCCACAGAGTCCCTTGTACATCTCATTTGGTTCACGG	5297
Sbjct	1561A.....	1620
Query	5298	ATGCCTTTTCAGGCAGGAATACAATGGCTTTGTACAATATACCGCTAGGGGGCAACTATTT	5357
Sbjct	1621	1680
Query	5358	CTGAGAAACTTGCCCGTACTGGCAACTAAAGTAAAAATGCTCATGGTAGGCAACCTTGGA	5417
Sbjct	1681	1740
Query	5418	GAAGAAATTGGTAATCTGGAACATCTTGGGTGGATCCTAAGGGGGCTGCCGTGTGTAAG	5477
Sbjct	1741	1800
Query	5478	AAGATCACAGAGCACGAAAAATGCCACATTAATATACTGGATAAACTAACCGCATTTTTTC	5537
Sbjct	1801	1860
Query	5538	GGGATCATGCCAAGGGGGACTACACCCAGAGCCCCGGTGAGGTTCCTACGAGCTTACTA	5597
Sbjct	1861	1920
Query	5598	AAAGTGAGGAGGGGTCTGGAGACTGGCTGGGCTTACACACACCAAGGCGGGATAAGTTCA	5657
Sbjct	1921	1980
Query	5658	GTCGACCATGTAACCGCCGGAAAAGATCTACTGGTCTGTGACAGCATGGGACGAACTAGA	5717
Sbjct	1981	2040
Query	5718	GTGGTTTGCCAAAGCAACAACAGGTTGACCGATGAGACAGAGTATGGCGTCAAGACTGAC	5777
Sbjct	2041	2100
Query	5778	TCAGGGTGCCCAGACGGTGCCAGATGTTATGTGTTAAATCCAGAGGCCGTTAACATATCA	5837
Sbjct	2101	2160
Query	5838	GGATCCAAAGGGGCAGTCGTTACCTCCAAAAGACAGGTGGAGAATTACGTTGTGCACC	5897
Sbjct	2161	2220
Query	5898	GCATCAGGCACACCGGCTTTCTTCGACCTAAAAAACTTGAAAGGATGGTCAGGCTTGCCT	5957
Sbjct	2221	2280
Query	5958	ATATTTGAAGCCTCCAGCGGGAGGGTGGTTGGCAGAGTCAAAGTAGGGAAGAATGAAGAG	6017
Sbjct	2281	2340
Query	6018	TCTAAACCTACAAAAATAATGAGTGGAATCCAGACCGTCTCAAAAAACACAGCAGACCTG	6077
Sbjct	2341	2400
Query	6078	ACCGAGATGGTCAAGAAGATAACCAGCATGAACAGGGGAGACTTCAAGCAGATTACTTTG	6137
Sbjct	2401C...	2460
Query	6138	GCAACAGGG-CAGGCAAAACACAGAACTCCCAAAAGCAGTTATAGAGGAGATAGGAAGA	6196
Sbjct	2461G.....	2520
Query	6197	CACAAGAGAGTATTAGTTCTTATACCATTAAGGGCAGCGGCAGAGTCAGTCTACCAGTAT	6256
Sbjct	2521C.....	2580
Query	6257	ATGAGATTGAAACACCCAAGCATCTCTTTTAACCTAAGGATAGGGGACATGAAAGAGGGG	6316
Sbjct	2581	2640

Query	6317	GACATGGCAACCGGGATAACCTATGCATCATACGGGTACTTCTGCCAAATGCCTCAACCA	6376
Sbjct	2641	2700
Query	6377	AAGCTCAGAGCTGCTATGGTAGAATACTCATACATATTCTTAGATGAATACCATTTGTGCC	6436
Sbjct	2701	2760
Query	6437	ACTCCTGAACAACTGGCAATTATCGGGAAGATCCACAGATTTTCAGAGAGTATAAGGGTT	6496
Sbjct	2761	2820
Query	6497	GTCGCCATGACTGCCACGCCAGCAGGGTCGGTGACCACAACAGGTCAAAGCACCCAATA	6556
Sbjct	2821	2880
Query	6557	GAGGAATTTCATAGCCCCGAGGTAATGAAAGGGGAGGATCTTGGTAGTCAGTTCCTTGAT	6616
Sbjct	2881	2940
Query	6617	ATAGCAGGGTTAAAAATACCAGTGGATGAGATGAAAGGCAATATGTTGGTTTTTGTACCA	6676
Sbjct	2941	3000
Query	6677	ACGAGAAACATGGCAGTAGAGGTAGCAAAGAAGCTAAAAGCTAAGGGCTATAACTCTGGA	6736
Sbjct	3001	3060
Query	6737	TACTATTACAGTGGAGAGGATCCAGCCAATCTGAGAGTTGTGACATCACAATCCCCCTAT	6796
Sbjct	3061	3120
Query	6797	GTAATCGTGGCTACAAATGCTATTGAATCAGGAGTGACACTACCAGATTTGGACACGGTT	6856
Sbjct	3121	3180
Query	6857	ATAGACACGGGGTTGAAATGTGAAAAGAGGGTGAGGGTATCATCAAAGATACCCCTTCATC	6916
Sbjct	3181G.....	3240
Query	6917	GTAACAGGCCTTAAGAGGATGGCCGTGACTGTGGGTGAGCAGGCGCAGCGTAGGGGCAGA	6976
Sbjct	3241	3300
Query	6977	GTAGGTAGAGTGAAACCCGGGAGGTATTATAGGAGCCAGGAAACAGCAACAGGGTCAAAG	7036
Sbjct	3301	3360
Query	7037	GACTACCACATATGACCTCTTGCAAGCACAAAGATACGGGATTGAGGATGGAATCAACGTG	7096
Sbjct	3361	3420
Query	7097	ACGAAATCCTTTAGGGAGATGAATTACGATTGGAGCCTATACGAGGAGGACAGCCTACTA	7156
Sbjct	3421	3480
Query	7157	ATAACCCAGCTGGAATACTAAATAATCTACTCATCTCAGAAGACTTGCCAGCCGCTGTT	7216
Sbjct	3481	3540
Query	7217	AAGAACATAATGGCCAGGACTGATCACCCAGAGCCAATCCAACCTTGCATACAACAGCTAT	7276
Sbjct	3541	3600
Query	7277	GAAGTCCAGGTCCCGTCTATTCCCAAAAATAAGGAATGGAGAAGTCACAGACACCTAC	7336
Sbjct	3601G.....	3660
Query	7337	GAAATTAATCTCGTTTCTAAATGCCAGAAAGTTAGGGGAGGATGTGCCCGTGATATCTAC	7396
Sbjct	3661	3720
Query	7397	GCTACTGAAGATGAGGATCTGGCAGTTGACCTCTTAGGGCTAGACTGGCCTGATCCTGGG	7456
Sbjct	3721	3780
Query	7457	AACCAGCAGGTAGTGGAGACTGGTAAAGCACTGAAGCAAGTGACCGGGTTGTCCTCGGCT	7516
Sbjct	3781	3840
Query	7517	GAAATGCCCTACTAGTGGCTTTATTTGGGTATGTGGGTACCAGGCTCTCTCAAAGAGG	7576
Sbjct	3841	3900

Query	7577	CATGTCCCAATGATAACAGACATATATACCATCGAGGACCAGAGACTAGAAGACACCACC	7636
Sbjct	3901	3960
Query	7637	CACCTCCAGTATGCACCCAACGCCATAAAAACCGATGGGACAGAGACTGAACTGAAAGAA	7696
Sbjct	3961	4020
Query	7697	CTGGCGTCGGGTGACGTGGAAAAAATCATGGGAGCCATTTTCTAGATTATGCAGCTGGGGGA	7756
Sbjct	4021	4080
Query	7757	CTGGAGTTTGTAAATCCCAAGCAGAAAAGATAAAAACAGCTCCTTTGTTTAAAGAAAAC	7816
Sbjct	4081	4140
Query	7817	GCAGAAGCCGCAAAAGGGTATGTCCAAAAATTCATTGACTCATTAATTGAAAATAAAGAA	7876
Sbjct	4141	.T.....T.....	4200
Query	7877	GAAATAATCAGATATGGTTTGTGGGGAACACACACAGCACTATACAAAAGCATAGCTGCA	7936
Sbjct	4201	4260
Query	7937	AGACTGGGGCATGAAACAGCGTTTGGCCACACTAGTGTTAAAGTGGCTAGCTTTTGGAGGG	7996
Sbjct	4261	4320
Query	7997	GAATCAGTGTCTAGACCACGTCAAGCAGGCGGCAGTTGATTTAGTGGTCTATTATGTGATG	8056
Sbjct	4321	4380
Query	8057	AATAAGCCTTCCTTCCCAGGTGACTCCGAGACACAGCAAGAAGGGAGGCGATTTCGTCGCA	8116
Sbjct	4381	4440
Query	8117	AGCCTGTTTCATCTCCGCACTGGCAACCTACACATACAAAACCTTGAATTACCACAATCTC	8176
Sbjct	4441G.....	4500
Query	8177	TCTAAAGTGGTGGAAAC-AGCCCTGGCTTACCTCCCCTATGCTACCAGCGCATTAATAATG	8235
Sbjct	4501C.....	4560
Query	8236	TTCACCCCAACGCGGCTGGAGAGCGTGGTGATACTGAGCACCACGATATATAAAACATAC	8295
Sbjct	4561	4620
Query	8296	CTCTCTATAAGGAAGGGGAAGAGTGATGGATTGCTGGGTACGGGGATAAGTGCAGCCATG	8355
Sbjct	4621	4680
Query	8356	GAAATCCTGTCACAAAACCCAGTATCGGTAGGTATATCTGTGATGTTGGGGGTAGGGGCA	8415
Sbjct	4681	4740
Query	8416	ATCGCTGCGCACAAACGCTATTGAGTCCAGTGAACAGAAAAGGACCCTACTTATGAAGGTG	8475
Sbjct	4741	4800
Query	8476	TTTGTAAAGAACTTCTTGGATCAGGCTGCAACAGATGAGCTGGTAAAAGAAAACCCAGAA	8535
Sbjct	4801	4860
Query	8536	AAAATTATAATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCTGAGACTAATA	8595
Sbjct	4861	4920
Query	8596	TACCACCTGTATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAACCTATCTGAGAGGACA	8655
Sbjct	4921	4980
Query	8656	GCAGGCAGAAACTTATTACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGAC	8715
Sbjct	4981	5040
Query	8716	TCACAAGGGAAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTA	8775
Sbjct	5041T.....	5100
Query	8776	CACAAGCAAATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCCCTGCACCCTTT	8835
Sbjct	5101	5160

Query	8836	AGTTGTGACTGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAACCTATTTGAGG	8895
Sbjct	5161	5220
Query	8896	GTAGAAACCAGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAA	8955
Sbjct	5221	5280
Query	8956	CTTACCAAAGTGGAGGAGAGCGGGCCTTTCCTATGTAGAAACAGACCTGGTAGGGGACCA	9015
Sbjct	5281	5340
Query	9016	GTCAACTACAGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCA	9075
Sbjct	5341	5400
Query	9076	AAGTTGGAAGGACAGGTAGAGCACTACTACAAAGGGGTACAGCAAAAATTGACTACAGT	9135
Sbjct	5401	5460
Query	9136	AAAGGAAAAATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGG	9195
Sbjct	5461	5520
Query	9196	TTAGCTAAGAGATATACTGGGGTCGGGTTCATGGTGCATACTTAGGTGACGAGCCCAAT	9255
Sbjct	5521	5580
Query	9256	CACCGTGCTCTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTA	9315
Sbjct	5581	5640
Query	9316	AAAATGAAGAAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTC	9375
Sbjct	5641	5700
Query	9376	ATCGAACTAGTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACC	9435
Sbjct	5701	5760
Query	9436	ACATGGCTAGCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGA	9495
Sbjct	5761	5820
Query	9496	GAGAGAGTAATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGAC	9555
Sbjct	5821	5880
Query	9556	ACGTCAGAGGTTGGGATCACAATAATTGGAAGGGAAACCCTGATGACAACGGGAGTGACA	9615
Sbjct	5881G.....	5940
Query	9616	CCTGTCTTGGAAAAAGTAGAGCCTGACGCCAGCGACAACCAAACTCGGTGAAGATCGGG	9675
Sbjct	5941	6000
Query	9676	TTGGATGAGGGTAATTACCCAGGGCCTGGAATACAGACACATACACTAACAGAAGAAATA	9735
Sbjct	6001	6060
Query	9736	CACAACAGGGATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATTCATATCAAAT	9795
Sbjct	6061	6120
Query	9796	AGGGCAAAGACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCCAGGGAAATACGA	9855
Sbjct	6121	6180
Query	9856	GACTTGATGGCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTCGACCCTGAGCTG	9915
Sbjct	6181	6240
Query	9916	TCTGAAATGGTCGATTTCAAGGGGACTTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGT	9975
Sbjct	6241	6300
Query	9976	CTCGGGCAACCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAG	10035
Sbjct	6301	6360
Query	10036	AAAAAAGATGTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTG	10095
Sbjct	6361	6420

Query	10096	GCCTTAAAAAATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCT	10155
Sbjct	6421G.....	6480
Query	10156	AAAGCACTTGGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTAT	10215
Sbjct	6481	6540
Query	10216	GCCATGAAGCTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCA	10274
Sbjct	6541T.C.....	6600
Query	10275	CTGTTTGAGGAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATG	10334
Sbjct	6601	6660
Query	10335	GCATCAGCTTACCAATTGGCACAGGGTAACTGGGAGCCCCTCGGTTGCGGGGTGCACCTA	10394
Sbjct	6661	6720
Query	10395	GGTACAATACCAGCCAGAAGGGTGAAGATACACCCATATGAAGCTTACCTGAAGTTGAAA	10454
Sbjct	6721	6780
Query	10455	GATTTTCATagaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCAC	10514
Sbjct	6781	6840
Query	10515	AACAAATGGATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTC	10574
Sbjct	6841	6900 \
Query	10575	AACCCAGGGAAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAAC	10634
Sbjct	6901T.....	6960
Query	10635	CACCAGATTGGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTG	10694
Sbjct	6961	7020
Query	10695	AGGGCCCCAAACCGACACCAAAACCTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGT	10754
Sbjct	7021A.....	7080
Query	10755	GAAAACCGGCAAAATCCAGAATTGCACAACAAATTGTTGGAGATTTCCACACGATAGCC	10814
Sbjct	7081	7140
Query	10815	CAACCCACCCTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGGTA	10874
Sbjct	7141G.....A..	7200
Query	10875	AATAGAAAGGGGCGAGCAGGCTTCCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTCA	10934
Sbjct	7201	7260
Query	10935	GAAAAGCACCTGGTAGAACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATAT	10994
Sbjct	7261	7320
Query	10995	TATGAAACTGCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGG	11054
Sbjct	7321	7380
Query	11055	GACCTGGTGGTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTA	11114
Sbjct	7381A.....	7440
Query	11115	GCCATCACTAAGGTCATGTATAACTGGGTGAAACAGCAGCCCGTTGTGATTCCAGGATAT	11174
Sbjct	7441	7500
Query	11175	GAAGGAAAGACCCCTTGTTCACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTC	11234
Sbjct	7501G.....T....	7560
Query	11235	AATGAGCCAGTGGCCGTAAGTTTTGACACCAAAGCCTGGGACACTCAAGTACTAGTAAG	11294
Sbjct	7561	7620
Query	11295	GATCTGCAACTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAGTTC	11354
Sbjct	7621	7680

Query	11355	ATTGACACCATCACCGACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTA	11414
Sbjct	7681A..	7740
Query	11415	TATATAAGAAATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATG	11474
Sbjct	7741	7800
Query	11475	TTAAATGTCCTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGT	11534
Sbjct	7801C.....	7860
Query	11535	TTCAACAGGGTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAA	11594
Sbjct	7861	7920
Query	11595	GGGTTAGGGCTGAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCT	11654
Sbjct	7921	7980
Query	11655	CAGAAGATAACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTC	11714
Sbjct	7981	8040
Query	11715	TGTTCTCATACCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGG	11774
Sbjct	8041	8100
Query	11775	AGAGACACCGCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGG	11834
Sbjct	8101	8160
Query	11835	GGTACCACAGCATATGAAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCCTGGAAC	11894
Sbjct	8161	8220
Query	11895	CCGCTTGTTAGGAGGATTTGCCTGTTGGTCCTTTCGCAACAGCCAGAGACAGACCCATCA	11954
Sbjct	8221	8280
Query	11955	AAACATGCCACTTATTATTACAAAGGTGATCCAATAGGGGCCTATAAAGATGTAATAGGT	12014
Sbjct	8281G.....	8340
Query	12015	CGGAATCTAAGTGAAGTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGC	12074
Sbjct	8341A.....	8400
Query	12075	CTGTCCACGTTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTCAGGACTGTGTT	12134
Sbjct	8401A.....	8460
Query	12135	GCCATTGGGAAAGAAGAGGGCAACTGGCTAGTTAA-GCCCGACAGGCTGATATCCAGCAA	12193
Sbjct	8461C...-.....	8519
Query	12194	AACTGGCCACTTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTTATGAGCA	12253
Sbjct	8520	8579
Query	12254	ACTGCAGCTAAGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTT	12312
Sbjct	8580G.....	8639
Query	12313	AGGTCCCATAGTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGG	12372
Sbjct	8640	8699
Query	12373	CGTCAGCAGCTGA	12385
Sbjct	8700	G.....	8712

>  gi|7960755|emb|AJ133739.1|BVI133739  Bovine viral diarrhea virus complete RNA g
isolate NADL
Length=12308

Score = 1.333e+04 bits (7218), Expect = 0.0
Identities = 7301/7316 (99%), Gaps = 6/7316 (0%)
Strand=Plus/Plus

Query	5301	CCTTTTCAGGCAGGAATACAATGGCTTTGTACAATATACCGCTAGGGGGCAACTATTTCTG	5360
Sbjct	4994	5053
Query	5361	AGAAACTTGCCCGTACTGGCAACTAAAGTAAAAATGCTCATGGTAGGCAACCTTGGAGAA	5420
Sbjct	5054	5113
Query	5421	GAAATTGGTAATCTGGAACATCTTGGGTGGATCCTAAGGGGGCCTGCCGTGTGTAAGAAG	5480
Sbjct	5114	5173
Query	5481	ATCACAGAGCACGAAAAATGCCACATTAATATACTGGATAAACTAACCGCATTTTTTCGGG	5540
Sbjct	5174	5233
Query	5541	ATCATGCCAAGGGGGACTACACCCAGAGCCCCGGTGAGGTTCCCTACGAGCTTACTAAAA	5600
Sbjct	5234	5293
Query	5601	GTGAGGAGGGGTCTGGAGACTGGCTGGGCTTACACACACCAAGGCGGGATAAGTTCAGTC	5660
Sbjct	5294	5353
Query	5661	GACCATGTAACCGCCGGAAGATCTACTGGTCTGTGACAGCATGGGACGAACTAGAGTG	5720
Sbjct	5354	5413
Query	5721	GTTTGCCAAAGCAACAACAGGTTGACCGATGAGACAGAGTATGGCGTCAAGACTGACTCA	5780
Sbjct	5414	5473
Query	5781	GGGTGCCCAGACGGTGCCAGATGTTATGTGTTAAATCCAGAGGCCGTTAACATATCAGGA	5840
Sbjct	5474	5533
Query	5841	TCCAAAGGGGCAGTCGTTTACCCTCCAAAAGACAGGTGGAGAATTACAGTGTGTCACCGCA	5900
Sbjct	5534	5593
Query	5901	TCAGGCACACCGGCTTTCTTCGACCTAAAAAATTGAAAGGATGGTCAGGCTTGCCTATA	5960
Sbjct	5594	5653
Query	5961	TTTGAAGCCTCCAGCGGGAGGGTGGTTGGCAGAGTCAAAGTAGGGAAGAATGAAGAGTCT	6020
Sbjct	5654	5713
Query	6021	AAACCTACAAAAATAATGAGTGGAATCCAGACCGTCTCAAAAAACACAGCAGACCTGACC	6080
Sbjct	5714	5773
Query	6081	GAGATGGTCAAGAAGATAACCAGCATGAACAGGGGAGACTTCAAGCAGATTACTTTGGCA	6140
Sbjct	5774	5833
Query	6141	ACAGGG-CAGGCAAAACCACAGAACTCCCAAAGCAGTTATAGAGGAGATAGGAAGACAC	6199
Sbjct	5834G.....	5893
Query	6200	AAGAGAGTATTAGTTCTTATACCATTAAGGGCAGCGGCAGAGTCAGTCTACCAGTATATG	6259
Sbjct	5894	5953
Query	6260	AGATTGAAACACCCAAGCATCTCTTTTAACCTAAGGATAGGGGACATGAAAGAGGGGGAC	6319
Sbjct	5954	6013
Query	6320	ATGGCAACCGGGATAACCTATGCATCATACGGGTACTTCTGCCAAATGCCTCAACCAAAG	6379
Sbjct	6014	6073
Query	6380	CTCAGAGCTGCTATGGTAGAATACTCATACATATTCTTAGATGAATACCATTTGTGCCACT	6439
Sbjct	6074	6133
Query	6440	CCTGAACAACTGGCAATTATCGGGAAGATCCACAGATTTTCAGAGAGTATAAGGGTTGTC	6499
Sbjct	6134	6193
Query	6500	GCCATGACTGCCACGCCAGCGGGTCGGTGACCACAACAGGTCAAAGCACCCAATAGAG	6559
Sbjct	6194	6253

Query	6560	GAATTCATAGCCCCCGAGGTAATGAAAGGGGAGGATCTTGGTAGTCAGTTCCTTGATATA	6619
Sbjct	6254	6313
Query	6620	GCAGGGTTAAAAATACCAGTGGATGAGATGAAAGGCAATATGTTGGTTTTTGTACCAACG	6679
Sbjct	6314	6373
Query	6680	AGAAACATGGCAGTAGAGGTAGCAAAGAAGCTAAAAGCTAAGGGCTATAACTCTGGATAC	6739
Sbjct	6374	6433
Query	6740	TATTACAGTGGAGAGGATCCAGCCAATCTGAGAGTTGTGACATCACAATCCCCCTATGTA	6799
Sbjct	6434	6493
Query	6800	ATCGTGGCTACAAATGCTATTGAATCAGGAGTGACACTACCAGATTTGGACACGGTTATA	6859
Sbjct	6494	6553
Query	6860	GACACGGGGTTGAAATGTGAAAAGAGGGTGAGGGTATCATCAAAGATACCCCTTCATCGTA	6919
Sbjct	6554	6613
Query	6920	ACAGGCCTTAAGAGGATGGCCGTGACTGTGGGTGAGCAGGCGCAGCGTAGGGGCAGAGTA	6979
Sbjct	6614	6673
Query	6980	GGTAGAGTGAAACCCGGGAGGTATTATAGGAGCCAGGAAACAGCAACAGGGTCAAAGGAC	7039
Sbjct	6674	6733
Query	7040	TACCACATGACCTCTTGCAGGCACAAAGATACGGGATTGAGGATGGAATCAACGTGACG	7099
Sbjct	6734	.T.....	6793
Query	7100	AAATCCTTTAGGGAGATGAATTACGATTGGAGCCTATACGAGGAGGACAGCCTACTAATA	7159
Sbjct	6794	6853
Query	7160	ACCCAGCTGGAAATACTAAATAATCTACTCATCTCAGAAGACTTGCCAGCCGCTGTTAAG	7219
Sbjct	6854	6913
Query	7220	AACATAATGGCCAGGACTGATCACCAGAGCCAATCCAACCTTGCATACAACAGCTATGAA	7279
Sbjct	6914	6973
Query	7280	GTCCAGGTCCCGGTCCTATTCCCAAAAATAAGGAATGGAGAAGTACAGACACCTACGAA	7339
Sbjct	6974G.....	7033
Query	7340	AATTACTCGTTTCTAAATGCCAGAAAGTTAGGGGAGGATGTGCCCGTGTATATCTACGCT	7399
Sbjct	7034	7093
Query	7400	ACTGAAGATGAGGATCTGGCAGTTGACCTCTTAGGGCTAGACTGGCCTGATCCTGGGAAC	7459
Sbjct	7094	7153
Query	7460	CAGCAGGTAGTGGAGACTGGTAAAGCACTGAAGCAAGTGACCGGGTTGTCCTCGGCTGAA	7519
Sbjct	7154	7213
Query	7520	AATGCCCTACTAGTGGCTTTATTTGGGTATGTGGGTACCAGGCTCTCTCAAAGAGGCAT	7579
Sbjct	7214	7273
Query	7580	GTCCCAATGATAACAGACATATATACCATCGAGGACCAGAGACTAGAAGACACCACCAC	7639
Sbjct	7274	7333
Query	7640	CTCCAGTATGCACCCAACGCCATAAAAACCGATGGGACAGAGACTGAACTGAAAGAAGT	7699
Sbjct	7334	7393
Query	7700	GCGTCGGGTGACGTGGAAAAAATCATGGGAGCCATTTTCAGATTATGCAGCTGGGGGACTG	7759
Sbjct	7394	7453
Query	7760	GAGTTTGTAAATCCCAAGCAGAAAAGATAAAAACAGCTCCTTTGTTTAAAGAAAACGCA	7819
Sbjct	7454	7513

Query	7820	GAAGCCGCAAAAGGGTATGTCCAAAATTCATTGACTCATTAATTGAAAATAAAGAAGAA	7879
Sbjct	7514	7573
Query	7880	ATAATCAGATATGGTTTGTGGGGAACACACACAGCACTATACAAAAGCATAGCTGCAAGA	7939
Sbjct	7574	7633
Query	7940	CTGGGGCATGAAACAGCGTTTGCCACACTAGTGTTAAAGTGGCTAGCTTTTGGAGGGGAA	7999
Sbjct	7634	7693
Query	8000	TCAGTGTGACACCACGTCAAGCAGGCGGCAGTTGATTTAGTGGTCTATTATGTGATGAAT	8059
Sbjct	7694	7753
Query	8060	AAGCCTTCCTTCCCAGGTGACTCCGAGACACAGCAAGAAGGGAGGCGATTTCGTCGCAAGC	8119
Sbjct	7754	7813
Query	8120	CTGTTTCATCTCCGCACTGGCAACCTACACATACAAAACCTTGAATTACCACAATCTCTCT	8179
Sbjct	7814	7873
Query	8180	AAAGTGGTGGAAC-AGCCCTGGCTTACCTCCCCTATGCTACCAGCGCATTAAAAATGTTC	8238
Sbjct	7874 C	7933
Query	8239	ACCCCAACGCGGCTGGAGAGCGTGGTGATACTGAGCACCACGATATATAAAACATACCTC	8298
Sbjct	7934	7993
Query	8299	TCTATAAGGAAGGGGAAGAGTGATGGATTGCTGGGTACGGGGATAAGTGCAGCCATGGAA	8358
Sbjct	7994	8053
Query	8359	ATCCTGTCACAAAACCCAGTATCGGTAGGTATATCTGTGATGTTGGGGGTAGGGGCAATC	8418
Sbjct	8054	8113
Query	8419	GCTGCGCACAAACGCTATTGAGTCCAGTGAACAGAAAAGGACCCTACTTATGAAGGTGTTT	8478
Sbjct	8114	8173
Query	8479	GTAAAGAACTTCTTGGATCAGGCTGCAACAGATGAGCTGGTAAAAGAAAACCCAGAAAAA	8538
Sbjct	8174	8233
Query	8539	ATTATAATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCCTGAGACTAATATAC	8598
Sbjct	8234	8293
Query	8599	CACCTGTATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAACTATCTGAGAGGACAGCA	8658
Sbjct	8294	8353
Query	8659	GGCAGAACTTATTACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGACTCA	8718
Sbjct	8354	8413
Query	8719	CAAGGGAAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTACAC	8778
Sbjct	8414	8473
Query	8779	AAGCAAATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCCTGCACCCTTTAGT	8838
Sbjct	8474	8533
Query	8839	TGTGACTGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAACCTATTTGAGGGTA	8898
Sbjct	8534	8593
Query	8899	GAAACCAGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAACCTT	8958
Sbjct	8594	8653
Query	8959	ACCAAAGTGGAGGAGAGCGGGCCTTTCCTATGTAGAAACAGACCTGGTAGGGGACCAGTC	9018
Sbjct	8654	8713
Query	9019	AACTACAGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCAAAG	9078
Sbjct	8714	8773

Query	9079	TTGGAAGGACAGGTAGAGCACTACTACAAAGGGGTCACAGCAAAAATTGACTACAGTAAA	9138
Sbjct	8774	8833
Query	9139	GGAAAAATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGGTTA	9198
Sbjct	8834	8893
Query	9199	GCTAAGAGATATACTGGGGTCGGGTTCAATGGTGCATACTTAGGTGACGAGCCCAATCAC	9258
Sbjct	8894	8953
Query	9259	CGTGCTCTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTAAAA	9318
Sbjct	8954	9013
Query	9319	ATGAAGAAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTCATC	9378
Sbjct	9014	9073
Query	9379	GAAGTAGTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACCACA	9438
Sbjct	9074	9133
Query	9439	TGGCTAGCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGAGAG	9498
Sbjct	9134	9193
Query	9499	AGAGTAATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGACACG	9558
Sbjct	9194	9253
Query	9559	TCAGAGGTTGGGATCACAATAATTGGAAGGGAACCCTGATGACAACGGGAGTGACACCT	9618
Sbjct	9254	9313
Query	9619	GTCTTGGA AAAAGTAGAGCCTGACGCCAGCGACAACCAAAACTCGGTGAAGATCGGGTTG	9678
Sbjct	9314	9373
Query	9679	GATGAGGGTAATTACCCAGGGCCTGGAATACAGACACATACTAACAGAAGAAATACAC	9738
Sbjct	9374	9433
Query	9739	AACAGGGATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATCCATATCAAATAGG	9798
Sbjct	9434	9493
Query	9799	GCAAAGACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCAGGGAAATACGAGAC	9858
Sbjct	9494	9553
Query	9859	TTGATGGCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTCGACCCTGAGCTGTCT	9918
Sbjct	9554	9613
Query	9919	GAAATGGTCGATTTCAAGGGGACTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGTCTC	9978
Sbjct	9614	9673
Query	9979	GGGCAACCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAGAAA	10038
Sbjct	9674	9733
Query	10039	AAAGATGTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTGGCC	10098
Sbjct	9734	9793
Query	10099	TTAAAAAATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCTAAA	10158
Sbjct	9794 G	9853
Query	10159	GCACCTGGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTATGCC	10218
Sbjct	9854	9913
Query	10219	ATGAAGCTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCACTG	10277
Sbjct	9914 T.C	9973
Query	10278	TTTGAGGAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATGGCA	10337
Sbjct	9974	10033

Query	10338	TCAGCTTACCAATTGGCACAGGGTAACTGGGAGCCCCTCGGTTGCGGGGTGCACCTAGGT	10397
Sbjct	10034	10093
Query	10398	ACAATACCAGCCAGAAGGGTGAAGATACACCCATATGAAGCTTACCTGAAGTTGAAAGAT	10457
Sbjct	10094	10153
Query	10458	TTCATagaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCACAAC	10517
Sbjct	10154	10213
Query	10518	AAATGGATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTCAAC	10577
Sbjct	10214	10273
Query	10578	CCAGGGAAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAACCAC	10637
Sbjct	10274	..T.....	10333
Query	10638	CAGATTGGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTGAGG	10697
Sbjct	10334	10393
Query	10698	GCCCAAACCGACACCAAAACCTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGTGAA	10757
Sbjct	10394	10453
Query	10758	AACCGGCAAAATCCAGAATTGCACAACAAATTGTTGGAGATTTCCACACGATAGCCCAA	10817
Sbjct	10454	10513
Query	10818	CCCACCCTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGTAAAT	10877
Sbjct	10514A.....	10573
Query	10878	AGAAAGGGGGCAGCAGGCTTCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTGAGAA	10937
Sbjct	10574	10633
Query	10938	AAGCACCTGGTAGACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATATTAT	10997
Sbjct	10634	10693
Query	10998	GAAACTGCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGGGAC	11057
Sbjct	10694	10753
Query	11058	CTGGTGGTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTAGCC	11117
Sbjct	10754	10813
Query	11118	ATCACTAAGGTCATGTATAACTGGGTGAAACAGCAGCCCCTTGTGATTCCAGGATATGAA	11177
Sbjct	10814	10873
Query	11178	GGAAAGACCCCCTTGTTCACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTCAAT	11237
Sbjct	10874	10933
Query	11238	GAGCCAGTGGCCGTAAGTTTTGACACCAAAGCCTGGGACACTCAAGTGACTAGTAAGGAT	11297
Sbjct	10934	10993
Query	11298	CTGCAACTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAGTTCATT	11357
Sbjct	10994	11053
Query	11358	GACACCATCACCGACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTATAT	11417
Sbjct	11054	11113
Query	11418	ATAAGAAATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATGTTA	11477
Sbjct	11114	11173
Query	11478	AATGTCCTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGTTTC	11537
Sbjct	11174C.....	11233
Query	11538	AACAGGGTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAAGGG	11597
Sbjct	11234	11293

Query	11598	TTAGGGCT ² GAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCTCAG	11657
Sbjct	11294	11353
Query	11658	AAGATAACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTCTGT	11717
Sbjct	11354	11413
Query	11718	TCTCATACCCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGA	11777
Sbjct	11414	11473
Query	11778	GACACCGCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGT	11837
Sbjct	11474	11533
Query	11838	ACCACAGCATATGAAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCTTGGAACCCG	11897
Sbjct	11534 T	11593
Query	11898	CTTGTTAGGAGGATTTGCCTGTTGGTCCTTTCGCAACAGCCAGAGACAGACCCATCAAAA	11957
Sbjct	11594	11653
Query	11958	CATGCCACTTATTATTACAAAGGTGATCCAATAGGGGCCATAAAGATGTAATAGGTCGG	12017
Sbjct	11654	11713
Query	12018	AATCTAAGTGAAGTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTG	12077
Sbjct	11714	11773
Query	12078	TCCACGTTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTGAGGACTGTGTTGCC	12137
Sbjct	11774 A	11833
Query	12138	ATTGGGAAAGAAGAGGGCAACTGGCTAGTTAA-GCCCGACAGGCTGATATCCAGCAAAAC	12196
Sbjct	11834 C	11892
Query	12197	TGGCCACTTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACT	12256
Sbjct	11893	11952
Query	12257	GCAGCTAAGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTTAGG	12315
Sbjct	11953 G	12012
Query	12316	TCCCATAGTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGT	12375
Sbjct	12013	12072
Query	12376	CAGCAGCTGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATAT	12435
Sbjct	12073	12132
Query	12436	AAATATAGTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACA	12495
Sbjct	12133	12192
Query	12496	GTAGTCAAGATTATCTACCTCAAGATAACACTACATTTAATGCACACAGCACTTTAGCTG	12555
Sbjct	12193	12252
Query	12556	TATGAGGATACGCCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAGCCCCC	12611
Sbjct	12253	12308

Score = 7494 bits (4058), Expect = 0.0
 Identities = 4089/4104 (99%), Gaps = 2/4104 (0%)
 Strand=Plus/Plus

Query	929	TCAGACACGAAAGAAGAGGGAGCAACAAAAAGAAAACACAGAAACCCGACAGACTAGAA	988
Sbjct	890	949
Query	989	AGGGGGAAAATGAAAATAGTGCCCAAAGAATCTGAAAAAGACAGCAAAACTAAACCTCCG	1048
Sbjct	950	1009

Query	1049	GATGCTACAATAGTGGTGGGAAGGAGTCAAATACCAGGTGAGGAAGAAGGGAAAAACCAAG	1108
Sbjct	1010	1069
Query	1109	AGTAAAAACACTCAGGACGGCTTGTACCATAACAAAAACAAACCTCAGGAATCACGCAAG	1168
Sbjct	1070	1129
Query	1169	AAACTGGAAAAAGCATTGTTGGCGTGGGCAATAATAGCTATAGTTTTGTTTCAAGTTACA	1228
Sbjct	1130	1189
Query	1229	ATGGGAGAAAACATAACACAGTGAACCTACAAGATAATGGGACGGAAGGGATACAACGG	1288
Sbjct	1190	1249
Query	1289	GCAATGTTCCAAAGGGGTGTGAATAGAAGTTTACATGGAATCTGGCCAGAGAAAATCTGT	1348
Sbjct	1250	1309
Query	1349	ACTGGCGTCCCTTCCCATCTAGCCACCGATATAGAACTAAAAACAATTTCATGGTATGATG	1408
Sbjct	1310T.....	1369
Query	1409	GATGCAAGTGAGAAGACCAACTACACGTGTTGCAGACTTCAACGCCATGAGTGAACAAG	1468
Sbjct	1370	1429
Query	1469	CATGGTTGGTGCAACTGGTACAATATTGAACCCTGGATTCTAGTCATGAATAGAACCCAA	1528
Sbjct	1430	1489
Query	1529	GCCAATCTCACTGAGGGACAACCACCAAGGGAGTGCGCAGTCACTTGTAGGTATGATAGG	1588
Sbjct	1490	1549
Query	1589	GCTAGTGACTTAAACGTGGTAACACAAGCTAGAGATAGCCCCACACCCTTAACAGGTTGC	1648
Sbjct	1550	1609
Query	1649	AAGAAAGGAAAGAACTTCTCCTTTGCAGGCATATTGATGCGGGGCCCCTGCAACTTTGAA	1708
Sbjct	1610	1669
Query	1709	ATAGCTGCAAGTGATGTATTATTCAAAGAACATGAACGCATTAGTATGTTCCAGGATACT	1768
Sbjct	1670	1729
Query	1769	ACTCTTTACCTTGTGACGGGTGACCAACTCCTTAGAAGGTGCCAGACAAGGAACCGCT	1828
Sbjct	1730	1789
Query	1829	AAACTGACAACCTGGTTAGGCAAGCAGCTCGGGATACTAGGAAAAAAGTTGGAAAACAAG	1888
Sbjct	1790	1849
Query	1889	AGTAAGACGTGGTTTGGAGCATACGCTGCTTCCCCTTACTGTGATGTCGATCGCAAAATT	1948
Sbjct	1850	1909
Query	1949	GGCTACATATGGTATACAAAAAATTGCACCCCTGCCTGCTTACCCAAGAACACAAAAATT	2008
Sbjct	1910	1969
Query	2009	GTCGGCCCTGGGAAATTTGACACCAATGCAGAGGACGGCA-GATATTACATGAGATGGGG	2067
Sbjct	1970A.....	2029
Query	2068	GGTCACTTGTTCGGAGGTACTACTACTTTCTTTAGTGGTGTGTCCGACTTCGCACCGGAA	2127
Sbjct	2030	2089
Query	2128	ACAGCTAGTGTAATGTACCTAATCCTACATTTTCCATCCCACAAAGTCACGTTGATGTA	2187
Sbjct	2090	2149
Query	2188	ATGGATTGTGATAAGACCCAGTTGAACCTCACAGTGGAGCTGACAACAGCTGAAGTAATA	2247
Sbjct	2150T.....	2209
Query	2248	CCAGGGTCGGTCTGGAATCTAGGCAAATATGTATGTATAAGACCAAATTGGTGGCCTTAT	2307
Sbjct	2210	..T..A..A.....C.....GG.....	2269

Query	2308	GAGACAACTGTAGTGTGGCATTGGAAGAGGTGAGCCAGGTGGTGAAGTTAGTGTGAGG	2367
Sbjct	2270G.....	2329
Query	2368	GCACTCAGAGATTTAACACGCATTTGGAACGCTGCAACAACACTACTGCTTTTTTAGTATGC	2427
Sbjct	2330G.....C...A.....	2389
Query	2428	CTTGTTAAGATAGTCAGGGGCCAGATGGTACAGGGCATTCTGTGGCTACTATTGATAACA	2487
Sbjct	2390C.....	2449
Query	2488	GGGGTACAAGGGCACTTGGATTGCAAACCTGAATTCTCGTATGCCATAGCAAAGGACGAA	2547
Sbjct	2450	2509
Query	2548	AGAATTGGTCAACTGGGGGCTGAAGGCCTTACCACCACTTGAAGGAATACTCACCTGGA	2607
Sbjct	2510	2569
Query	2608	ATGAAGCTGGAAGACACAATGGTCATTGCTTGGTGCGAAGATGGGAAGTTAATGTACCTC	2667
Sbjct	2570	2629
Query	2668	CAAAGATGCACGAGAGAAACCAGATATCTCGCAATCTTGCATACAAGAGCCTTGCCGACC	2727
Sbjct	2630	2689
Query	2728	AGTGTGGTATTCAAAAACTCTTTGATGGGCGAAAGCAAGAGGATGTAGTCGAAATGAAC	2787
Sbjct	2690	2749
Query	2788	GACAACTTTGAATTTGGACTCTGCCCATGTGATGCCAAACCCATAGTAAGAGGGAAGTTC	2847
Sbjct	2750	2809
Query	2848	AATACAACGCTGCTGAACGGACCGGCCTTCCAGATGGTATGCCCCATAGGATGGACAGGG	2907
Sbjct	2810	2869
Query	2908	ACTGTAAGCTGTACGTCATTCAATATGGACACCTTAGCCACAACGTGGTACGGACATAT	2967
Sbjct	2870	2929
Query	2968	AGAAGGTCTAAACCATTCCCTCATAGGCAAGGCTGTATCACCCAAAAGAATCTGGGGGAG	3027
Sbjct	2930	2989
Query	3028	GATCTCCATAACTGCATCCTTGGAGGAAATTGGACTTGTGTGCCTGGAGACCAACTACTA	3087
Sbjct	2990	3049
Query	3088	TACAAAGGGGGCTCTATTGAATCTTGCAAGTGGTGTGGCTATCAATTTAAAGAGAGTGAG	3147
Sbjct	3050	3109
Query	3148	GGACTACCACACTACCCCATTTGGCAAGTGTAATTTGGAGAACGAGACTGGTTACAGGCTA	3207
Sbjct	3110	3169
Query	3208	GTAGACAGTACCTCTTGCAATAGAGAAGGTGTGGCCATAGTACCACAAGGGACATTAAAG	3267
Sbjct	3170	3229
Query	3268	TGCAAGATAGGAAAAACAACGTACAGGTATAGCTATGGATACCAAACTCGGACCTATG	3327
Sbjct	3230	3289
Query	3328	CCTTGCAGACCATATGAAATCATATCAAGTGAGGGGCTGTAGAAAAGACAGCGTGTACT	3387
Sbjct	3290	3349
Query	3388	TTCAACTACACTAAGACATTAAAAAATAAGTATTTTGAAGCCAGAGACAGCTACTTTTCAAG	3447
Sbjct	3350	3409
Query	3448	CAATACATGCTAAAAGGAGAGTATCAATACTGGTTTGACCTGGAGGTGACTGACCATCAC	3507
Sbjct	3410	3469
Query	3508	CGGGATTACTTCGCTGAGTCCATATTAGTGGTGGTAGTAGCCCTCTGGGTGGCAGATAT	3567
Sbjct	3470	3529

Query	3568	GTACTTTGGTTACTGGTTACATACATGGTCTTATCAGAACAGAAGGCCTTAGGGATTTCAG	3627
Sbjct	3530	3589
Query	3628	TATGGATCAGGGGAAGTGGTGATGATGGGCAACTTGCTAACCCATAACAATATTGAAGTG	3687
Sbjct	3590	3649
Query	3688	GTGACATACTTCTTGCTGCTGTACCTACTGCTGAGGGAGGAGAGCGTAAAGAAGTGGGTC	3747
Sbjct	3650	3709
Query	3748	TTACTCTTATACCACATCTTAGTGGTACACCCAATCAAATCTGTAATTGTGATCCTACTG	3807
Sbjct	3710	3769
Query	3808	ATGATTGGGGATGTGGTAAAGGCCGATTTCAGGGGGCCAAGAGTACTTGGGGAAAATAGAC	3867
Sbjct	3770	3829
Query	3868	CTCTGTTTTTACAACAGTAGTACTAATCGTCATAGGTTTAATCATAGCCAGGCGTGACCCA	3927
Sbjct	3830	3889
Query	3928	ACTATAGTGCCACTGGTAACAATAATGGCAGCACTGAGGGTCACTGAACTGACCCACCAG	3987
Sbjct	3890	3949
Query	3988	CCTGGAGTTGACATCGCTGTGGCGGTCATGACTATAACCCTACTGATGGTTAGCTATGTG	4047
Sbjct	3950	4009
Query	4048	ACAGATTATTTTAGATATAAAAAATGGTTACAGTGCATTCTCAGCCTGG-ATCTGGGGTG	4106
Sbjct	4010T.....	4069
Query	4107	TTCTTGATAAGAAGCCTAATATACCTAGGTAGAATCGAGATGCCAGAGGTAACATATCCCA	4166
Sbjct	4070	4129
Query	4167	AACTGGAGACCACTAACTTTAATACTATTATATTTGATCTCAACAACAATTGTAACGAGG	4226
Sbjct	4130	4189
Query	4227	TGGAAGGTTGACGTGGCTGGCCTATTGTTGCAATGTGTGCCTATCTTATTGCTGGTCACA	4286
Sbjct	4190	4249
Query	4287	ACCTTGTGGGCCGACTTCTTAACCCTAATACTGATCCTGCCTACCTATGAATTGGTTAAA	4346
Sbjct	4250	4309
Query	4347	TTATACTATCTGAAAACCTGTTAGGACTGATATAGAAAGAAGTTGGCTAGGGGGGATAGAC	4406
Sbjct	4310	4369
Query	4407	TATACAAGAGTTGACTCCATCTACGACGTTGATGAGAGTGGAGAGGGCGTATATCTTTTTT	4466
Sbjct	4370	4429
Query	4467	CCATCAAGGCAGAAAGCACAGGGGAATTTTTCTATACCTTGCCCCCTTATCAAAGCAACA	4526
Sbjct	4430	4489
Query	4527	CTGATAAGTTGCGTCAGCAGTAAATGGCAGCTAATATACATGAGTTACTTAACTTTGGAC	4586
Sbjct	4490	4549
Query	4587	TTTATGTACTACATGCACAGGAAAGTTATAGAAGAGATCTCAGGAGGTACCAACATAATA	4646
Sbjct	4550	4609
Query	4647	TCCAGGTTAGTGGCAGCACTCATAGAGCTGAACTGGTCCATGGAAGAAGAGGAGAGCAAA	4706
Sbjct	4610	4669
Query	4707	GGCTTAAAGAAGTTTTATCTATTGTCTGGAAGGTTGAGAAACCTAATAATAAAACATAAG	4766
Sbjct	4670	4729
Query	4767	GTAAGGAATGAGACCGTGGCTTCTTGGTACGGGGAGGAGGAAGTCTACGGTATGCCAAAG	4826
Sbjct	4730	4789

Query	4827	ATCATGACTATAATCAAGGCCAGTACACTGAGTAAGAGCAGGCACTGCATAATATGCACT	4886
Sbjct	4790	4849
Query	4887	GTATGTGAGGGCCGAGAGTGGAAAGGTGGCACCTGCCCAAATGTGGACGCCATGGGAAG	4946
Sbjct	4850	4909
Query	4947	CCGATAACGTGTGGGATGTCGCTAGCAGATTTCTGAAGAAAGACACTATAAAAGAATCTTT	5006
Sbjct	4910	4969
Query	5007	ATAAGGGAAGGCAACTTTGAGGGT	5030
Sbjct	4970	4993

Score = 1284 bits (695), Expect = 0.0
Identities = 695/695 (100%), Gaps = 0/695 (0%)
Strand=Plus/Plus

Query	1	GTATACGAGAATTAGAAAAGGCACTCGTATACGTATTGGGCAATTAAAAATAATAATTAG	60
Sbjct	1	60
Query	61	GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG	120
Sbjct	61	120
Query	121	GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA	180
Sbjct	121	180
Query	181	GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG	240
Sbjct	181	240
Query	241	ACGAGGGCATGCCCAAAGCACATCTTAACCTGAGCGGGGGTCGCCCAGGTAAAAGCAGTT	300
Sbjct	241	300
Query	301	TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCACTGTATTGCTAC	360
Sbjct	301	360
Query	361	TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAACTTTTATACAAAAC	420
Sbjct	361	420
Query	421	ATACAAACAAAAACCCGTCGGGGTGGAGGAACCTGTTTATGATCAGGCAGGTGATCCCTT	480
Sbjct	421	480
Query	481	ATTTGGTGAAAGGGGAGCAGTCCACCCTCAATCGACGCTAAAGCTCCACACAAGAGAGG	540
Sbjct	481	540
Query	541	GGAACGCGATGTTCCAACCAACTTGGCATCCTTACCAAAAAGAGGTGACTGCAGGTCGGG	600
Sbjct	541	600
Query	601	TAATAGCAGAGGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGA	660
Sbjct	601	660
Query	661	CTATAAAGGTCCCGTCTATCACAGGGCCCCGCTGG	695
Sbjct	661	695

> [gi|71727706|gb|DQ088995.1|](#) **D** Bovine viral diarrhea virus 1 strain Singer_Arg, co
Length=12236

Score = 1.182e+04 bits (6401), Expect = 0.0
Identities = 6978/7238 (96%), Gaps = 13/7238 (0%)
Strand=Plus/Minus

Query	5301	CCTTTTCAGGCAGGAATACAATGGCTTTGTACAATATACCGCTAGGGGGCAACTATTTCTG	5360
Sbjct	7248A.....T..C..G..	7189